Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

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The present sequence is that of a peptide comprising amino acid residues 403-422 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SX13 ADD349. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide cales II protein-binding GbpB peptides covalently linked with peptide abounds (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be
                  Streptoco
Streptoco
                                                  Streptoco
Streptoco
S agalact
Streptoco
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Streptoco
                                                                                                                                                      Streptoco
S. pyogen
Microbial
                                                                                                                                                                                                                                             Human G p
M. xanthu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                    Aminopept
                                                                                                                                                                                                                                                                                                       Aeromonas
                                                                                                                                                                                                                                                                                                                     Aeromonas
                                                                                                                                                                                                                                                                                                                                                          Aeromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                             Microbial
                                                                                                                                                                                                                                Microbial
                                                Abp29842
Abp27864
Adu69652
Adv88318
Adv81739
Adv79571
                                                                                                                                                      Abp25919
Adr83884
Abc91642
Abc91642
Abc91642
Abw9320
Abw9320
Abw93264
Abw87588
Aay87588
Aay87588
Aay87588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans glucan binding protein-B peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                             AAU19320
ABM94545
                                                                                                                    ADV81739
ADV79571
                                                                                                                                                        ABP25919
                                                                                                       ADV88318
                                                                                                                                                                            ADR83884
                                                                                       ADU69652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD93642 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 10; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2003; 2003WO-US006962
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08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-845091/78.
WO2003075845-A2
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Smith DJ,
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                                                                                                                   February 15, 2006, 22:17:24; Search time 183 Seconds (without alignments) 48.020 Million cell updates/sec
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Novel
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Add93653
Adx37273
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Adx37276
Add93651
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Adx
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Add93649
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                  GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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                                                                                       sw model
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ADX37276
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ADD93651
ADD93652
ADX37274
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ADT50227
ADT50226
ADT50165
ADR94595
AEAS8465
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ADD93649
ADD93650
ADD93653
ADX37272
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ABP29684
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
geneseqp2005s:*
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Maximum Match 100%
Listing first 45 su
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geneseqp1990s:*
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geneseqp2001s:*
                                                                                       protein search, using
                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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Result

Matches

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                        Streptococcus mutans glucan binding protein-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37. .156
note= "HLA-binding peptide"
74. .193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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                                                           ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                              Streptococcus mutans.
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                                  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                 Gaps
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0
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microparticle; major histocompatibility complex; tooth disease.
                                                                                       Length 20;
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                                                                                                                                                                                                                                                                                                               Streptococcus mutant glucan binding protein B peptide #22.
                                                                                                               Indels
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                                                                                    100.0%; Score 116; DB 7;
100.0%; Pred. No. 2.3e-11;
ive 0; Mismatches 0;
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100.0%; Pred. No. 2.3e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 22; 73pp; English.
                                                                                                                                                                                                                                   ADX37265 standard; peptide; 20 AA.
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-MUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                                                                                                                                                       21-APR-2005 (first entry)
                                                                                                               20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans
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(TAUB/) TAUBMAN M A.
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                                                                                                   Local Similarity
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                                                            Sequence 20 AA;
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Matches
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Gaps

2003-845091/78

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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                                                                                                                                                                                         raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                 100.0%; Score 116; DB 7;
100.0%; Pred. No. 8.6e-10;
iive 0; Mismatches 0;
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                                                                     Claim 6; Page 7; 49pp; English.
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                                                                            Local Similarity
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         GENBANK; AY046410
                                                                                                                                                                                                                              Sequence 431 AA;
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SSM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental class II protein-binding GbpB peptides, especially HLA-binding peptides, cowpositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitches or multipitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in dental caries comprises a fragment of to a major histocompatibility complex caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. .. 0 Length 431; Length 431; Indels 100.0%; Score 116; DB 7; 100.0%; Pred. No. 8.6e-10; ive 0; Mismatches 0; 116; DB 7; No. 8.6e-10; Streptococcus mutans glucan binding protein-B. Score Pred. 1 Composition useful as vaccines for a glucan binding protein-B binding class II protein. ADD93653 standard; protein; 431 AA 403 QEANYAGNOSIGNÝRGWFNP 422 Claim 5; Page 8-9; 49pp; English. 20 . 0 100.0%; 07-MAR-2003; 2003WO-US006962. 07-MAR-2002; 2002US-0363209P. (first entry) Query Match 100. Best Local Similarity 100. Matches 20; Conservative Taubman MA; passive immunisation. passive immunisation. Streptococcus mutans (FORS-) FORSYTH INST Query Match Best Local Similarity GENBANK; AY046414 Sequence 431 AA; WO2003075845-A2. Sequence 431 AA; 29-JAN-2004 Smith DJ, ADD93653; RESULT 5 ADD93653 888888888888 ò ö The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. The Gaps . 0 Length 431; Indels

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New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
                                                             immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                              Streptococcus mutant glucan binding protein B variant #2.
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Pred. No. 8.6e-10;
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mammals against dental caries.
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-032399P-
07-MAR-2002; 2002US-04033939.
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(first entry)
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                                                                                                                    Streptococcus mutans
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TAUBMAN M A.
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nes 20; Conserv
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21-APR-2005
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(TAUB/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease.
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   Indels
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 Mismatches
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08-JAN-1999; 99US-0115142P.
12-ARR-1999; 99US-0029049.
07-MAR-2002; 2002US-0363209P.
08-MUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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   Conservative
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                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans.
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(TAUB/) TAUBMAN M A.
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Best Local Similarity
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Mismatches
                                       Claim 16; SEQ ID NO 210; 402pp; English
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1es 20; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer;
gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.
                                                                                                                                                             New composition comprising a fragment of a glucan binding protein-B (GDB) that binds to MrC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries
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                                                                                                                                                                                                                                                                                                                               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            algorithm; adhesin; pharmaceutical; vaccine; drug screening;
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100.0%; Pred. No. 8.6e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                Claim 3; SEQ ID NO 33; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AEB91500 standard; protein; 431 AA
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                           08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
09-MAR-2004; 2004US-00797821
                    98US-0081550P
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                      Taubman MA;
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                                                                                       (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                          WPI; 2005-151644/16.
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                                                                                                                                                                                                                                                                                                           Sequence 431 AA;
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                    13-APR-1998;
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                                                                                                                     Smith DJ,
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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network Software, training an artificial neural network MNN) for each of the computed five attributes, and identifying the adhesin and adhesin and adhesin and adhesin and adhesin network (RAN) for equal or greater than 0.51. Also claimed is a set of 274 annotated genes concing adhesin and adhesin-like proteins, having 274 fully defined 162-cc 1151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical defined 306-18876 base pairs (SEQ) ID NO: 659-763); a set of 279 annotated adhesin-like proteins, having 105 fully defined 33-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying adhesin and adhesin-like proteins for further testing in development of new vaccine forwulations custominated diseases caused by various pathogenic organisms. (M1) is useful for identifying putative adhesins that are important in drug addressing ulcer and uninary trace infections. (M1) identifies adhesins from addressing from the proteins in the custominary and preventing therapeutics for whooping cough, pneumonia, and diseases caused by various pathogenic organisms.
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Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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100.0%; Pred. No. 8.6e-10;
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covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of a antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in

passive immunisation

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Sequence 432

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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions compisse major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides,
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class II protein.
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                                                                                                                                                                     The present sequence is the protein sequence of the glucan binding protein—B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Dispitopic or multipitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies can be praised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gment of complex
Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 116; DB 7;
Pred. No. 8.6e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans glucan binding protein-B.
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binding protein-B binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD93652 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 QEANYAGNQSIGNYRGWFNP 423
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                                                                                                                             Claim 5; Page 8; 49pp; English
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100.0%;
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08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2003; 2003WO-US006962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taubman MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          passive immunisation
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nes 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENBANK; AY046413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003075845-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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                                                                                                                                                                                                                                                         immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
Length 432;
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                                                                                                                                                                                                                                  Streptococcus mutant glucan binding protein B variant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                           Indels
; DB 7;
8.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 116; DB 9;
100.0%; Pred. No. 8.6e-10;
ive 0; Mismatches 0;
                         Mismatches
100.0%; Score 116; 100.0%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 31; 73pp; English.
                                                                                                                                                    ADX37274 standard; protein; 432 AA
                                                                              423
                                                      1 QEANYAGNQSIGNYRGWFNP 20
                           ; 0
                                                                     404 QEANYAGNQSIGNYRGWFNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                                                                       (first entry)
                           20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taubman MA;
                                                                                                                                                                                                                                                                                                     Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMITH D J.
TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
              Similarity
                                                                                                                                                                                                                                                                                                                               US2005031633-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIT/) SMITH
(TAUB/) TAUBMA
                                                                                                                                                                                                                                                                                                                                                                                                              13-APR-1998;
                                                                                                                                                                                                       21-APR-2005
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                                                                                                                                                                             ADX37274;
Query Match
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               Local
               Best Loca
Matches
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The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae. The protein, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for serotyping or classifying infectious agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acids from Streptococcus pneumoniae - useful, e.g. for identifying anti-bacterial(s) for treatment and prevention of
                            open reading frame; antibacterial; infection;
                                                                                                                                                                                                                                                                   Lonetto MA, Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae type 4 strain protein from coding region #2326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96; DB 2; Length 132;
Pred. No. 3.5e-07;
Mismatches 0; Indels
 Streptococcus pneumoniae encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; type 4 strain
                                                                                                                                                                                                                                                                   Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU02747 standard; protein; 392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 47; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ESNYAGNRTIGNHRGWFNP 118
                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EANYAGNOSIGNYRGWFNP 20
                                                                                                                                                                                           96US-0029930P.
                                                                                                                                                               97WO-US019226.
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78.9%;
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Best Local Similarity '...
Best Local Similarity '...
TS; Conservative
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                                                                         Streptococcus pneumoniae
                                           prevention; meningitis.
                                                                                                                                                                                                                                                                     Hodgson JE,
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                                                                                                                                                                                                                                                                                   Zarfos PN;
                                                                                                                                                                                                                                                                                                                WPI; 1998-286586/25.
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV37344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 132 AA;
                             coding region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200277021-A2
                                                                                                                                                               27-OCT-1997;
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                                                                                                     WO9819689-A1
                                                                                                                                 14-MAY-1998.
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                                                                                                                                                                                                                                                                                                                                                                                           meningitis
                                                                                                                                                                                                                                                                 Black MT,
Reid RH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                       immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                             Streptococcus mutant glucan binding protein B variant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; SEQ ID NO 32; 73pp; English.
                                                                                                    ADX37275 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW60944 standard; protein; 132 AA
                 404 QEANYAGNQSIGNYRGWFNP 423
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363220P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                             (first entry)
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ses 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taubman MA;
                                                                                                                                                                                                                                                                      Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIT/) SMITH D J. (TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 432 AA;
                                                                                                                                                                                                                                                                                                  US2005031633-A1.
                                                                                                                                                               21-APR-2005
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Matches
                                                                      RESULT 14
AAW60944
ID AAW60
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Gaps

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Fraser C;

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable formath, or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the Expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS5654. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein binds one of the proteins. Composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence contained within a Streptococcus mucleic acid sequence, where the first primer is substantially complementary to the target sequence and where the parts of the primers having substantially complementary to the complement of the target sequence. Companies as substantially complementary to the complement of the target sequence companies as substantially complementary to the complement of the target sequence complementarity define the termini of the primers having substantially complementary to the complement of a streptococcus pneumoniae bacterium, where one or more genes econd molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus cand also useful in developing vaccins, diagnostics and antibodies. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cut frandardise OS field)
                                                                                                                                                                                                                                                                                                                                                                New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4652; 56pp; English.
                                                                      27-MAR-2002; 2002WO-IB002163.
                                                                                                                       27-MAR-2001; 2001GB-00007658.
                                                                                                                                                                                                                                           Masignani V, Tettelin H,
                                                                                                                                                                  (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                           WPI; 2003-040579/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ear infection.
                         03-OCT-2002
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Gaps .. 0 82.8%; Score 96; DB 6; Length 392; 78.9%; Pred. No. 1.3e-06; Live 4; Mismatches 0; Indels Query Match
Best Local Similarity 78.9
Matches 15; Conservative

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Search completed: February 15, 2006, 22:20:44 Job time : 185 secs

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5.1.7
Biocceleration Ltd.
GenCore version (c) 1993 - 2006
           Copyright
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OM protein - protein search, using sw model

February 15, 2006, 22:20:59; Search time 38 Seconds (without alignments) 50.640 Million cell updates/sec Run on:

US-10-797-821-22 116

1 QEANYAGNOSIGNYRGWFNP 20 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score	Query	Query Match Length	BB C	DI	ion
96	82.8	392	0 0	G95258	secreted 45 kd pro
22.5	47.4	332	1 (1	AC0260	tical ph
	43.1	1061	~	A40609	OmpA-related prote
47	40.5	261	~	S71364	ubiquinol-cytochro
47	40.5	837	Н	S54429	outer membrane ush
46	39.7	319		856523	dihydrodipicolinat
46	39.7	510	7	A98154	hypothetical prote
46	39.7	521	~	AC3134	hypothetical prote
46	39.7	619	٦	KSNCTO	-
46	39.7	619	ч	KSNCLT	laccase (EC 1.10.3
46	39.7	888	~	C90595	hypothetical prote
45.5	39.5	350	7	AG3425	iolE protein [impo
	39.5	350	7	AE2954	conserved hypothet
45.5	39.5	370	7	H98328	hypothetical prote
•	39.5	385	7	D41732	heterogeneous nucl
45	38.8	108	٦	KVMS73	Ig kappa chain V r
45	38.8	242	٦	F75433	probable phosphoes
45	38.8	514	N	B64634	hypothetical prote
45	38.8	514	7	E71880	probable outer mem
45	38.8	536	N	T36109	hypothetical prote
45	38.8	621	~	S72493	laccase (EC 1.10.3
45	38.8	714	7	A83314	probable chemotaxi
45	38.8	835	~	T06590	probable beta-gala
44.5	38.4	1059	~	E87058	isoleucyl-tRNA syn
44	37.9	43	N	S21065	Ig kappa chain V r
44	37.9	147	~	140625	hypothetical prote
44	37.9	237	~	F97109	uncharacterized pr
44	37.9	416	~	S09334	transcobalamin I p

hypothetical prote exoribonuclease RA	actinohivin precur endo-beta-1,6-gluc	Ig kappa chain pre Ig kappa chain pre	hypothetical prote	conserved hypother hypother hypothetical prote	HFLK protein [impo	proteinase chain h	glucarate denydrat	hypothetical prote	hypothetical prote	dnaK-type molecula	hypothetical prote
T16078 S20126	JC7622 S55325	S04936 PL0113	S50009	T26526	AG2827	E97605	22/61/	T15633	T27542	S78277	E84432
0.0	0.0	0 0	0 0	7 77	7	ο,	٠,	~	7	7	0
645 1006	160	125	137	340	372	373	451	516	548	614	929
37.9	37.5	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1
4 4	43.5	4 4 6 6	4.4 E c	4 4 5 6	43	43	43	43	43	43	43
30	33 33	3.4 5.4	36	38	39	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1
secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95258
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, F.
nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
Ajite: Compiete enione sequence ol a vituami isolare ol streptococcus pheumoniae. AjReference number: A95000; MUID:21357209; PMID:11463916
A,Accession: G95258
A;Stauus; preliminary a.m.lemie tyne: DNa
A, Residues: 1-392 < KUR>
A;Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI000051B81; GB:AE005672; I A:Rxnerimental squrce: strain TIGR4
C, Genetics:
A;Gene: SP2216
Query Match 82.8%; Score 96; DB 2; Length 392; Rest Lonal Similarity 78.9%; Pred No. 6.3e-07:
rative 4
 Qy 2 BANYAGNQSIGNYRGWFNP 20
Db 360 ESNYAGNRTIGNHRGWFNP 378

general stress protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6) (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004 (Spaces: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004 (Spaces: 23-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004 (Spaces: 23-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004 (Spaces: 23-Oct-2001 #sequence\_revision Jr., W.; Arnold, J.; Baszczak, L.; Burgett, S.; DeHofff, B.S.; Es e. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.M.; Winkler, M.E. (Spaces: 37-Spaces: 37-Spa

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AjGenome: nuclear (Superfamily: ubiquinol-cytochrome-c reductase (cytochrome cl) (complex III), iron-sulfu CjSuperfamily: ubiquinol-cytochrome-c reductase (cytochrome cl) (complex; metalloprotein; mitoc CjKeywords: 2Fe-25; electron transfer membrane-associated complex; metalloprotein; mitoc CjKeymords: 2Fe-25 electron faitochrome-c reductase iron-sulfur protein #status experiment F;194-241/Domain: Rieske [2Fe-25] homology «RSK»
F;204,206,223,226/Binding site: 2Fe-25 cluster (Cys, His, Cys, His) (covalent) #status predicted F;205-225/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyacession: S54429
R; van Ham, S.M.; van Alphen, L.; Mooi, F.R.; van Putten, J.P.M.
Mol. Microbiol. 13, 673-684, 1994
A; Title: The finbrial gene cluster of Haemophilus influenzae type b.
A; Title: The finbrial gene cluster of Haemophilus influenzae type b.
A; Tatus: S54429
A; Recession: S54429
A; Status: Danary; nucleic acid sequence not shown; translation not shown
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-837 < VANN
A; Residues: 1-837 < VANN
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C; Genetics:
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dihydrodipicolinate synthase homolog yjhH - Escherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 10-Sep-1999 #text_change 01-Mar-2002
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: S56523; D65243
R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Fitle: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8
A;Reference number: S56314; MUID:95334362; PMID:7610040
Identification, cDNA sequence and deduced amino acid sequence of the mitochondri
                                                                                     A Accession: $71364
A Molecule type: MRNA
A) Residues: 1-261 <ATT>
A) Residues: 1-261 <ATT>
A) Residues: 1-261 <ATT>
A) Cross-references: UNIPROT: Q42703; UNIPARC: UPI000009F24B; EMBL: X91795; NID: g1418673; PII
A) Reperimental source: strain CW15
A) RACCESSION: $7209
A) Molecule type: protein
A) Residues: 55-74 <ATY>
C) Genetics: C) Genetics: A CONTACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane usher protein hifC precursor - Haemophilus influenzae (strain AM30)
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.5%; Score 47; DB 2; Length 261; larity 77.8%; Pred. No. 12; Conservative 1; Mismatches 1; Indels
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                                 g and subunit interaction.
A;Reference number: S71364; MUID:96235247; PMID:8647127
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Pred. No. 41;
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Start codon: GTG
C,Superfamily: outer membrane
C,Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 GNYQGWFCP 224
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Matches
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S54429
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0260
R;Paraly J; Whomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davie, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MuID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <KUR>
A;Residues: 1-332 <KUR>
C;Genetics:
A;Genetics:
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A;Residues: 1-1061 <MARP
A;Cross-references: UNIPROT:P38370; UNIPARC:UPI0000130B6B; GB:S64103; NID:g402803; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:135644, NCBIP:135645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Myxococcus xanthus
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A40609
R;Martinez-Canamero, M.; Munoz-Dorado, J.; Farez-Vidal, E.; Inouye, M.; Inouye, S.
J. Bacteriol. 175, 4756-4763, 1993
A;Title: Oar, a 115-kilodalton membrane protein required for development of Myxococcus A;Reference number: A40609; MUID:93328680; PMID:8335633
A;Status: preliminary
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ubiquinol-cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur protein precursor - (ubiquinol-cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur protein
NyAlternate names: Rieske iron-sulfur protein
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Dates: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71364; $78209
R;Atteia, A.; Franzen, L.G.
Ejur. J. Biochem. 237, 792-799, 1996
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                                                                                                                                                                                                                                                                                                                                  hypothetical phage protein YPO2132 [imported] - Yersinia pestis (strain CO92)
                                                                   Gaps
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Pred. No. 18; 7; Indels
3; Mismatches 7; Indels
         Length 392;
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                  6,3e-07;
0; Indels
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Pred. No. 0.94;
         DB 2;
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                                                                      4; Mismatches
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OmpA-related protein Oar - Myxococcus xanthus
            Score 96;
Pred. No.
                                                                                                                                                               |:||||||::||||:
ESNYAGNRTIGNHRGWFNP 378
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844 QANYTWSRLYGNYPGLFRP 862
                                                                                                                          2 EANYAGNOSIGNYRGWFNP 20
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            82.8%;
78.9%;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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                                                                      15; Conservative
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Best Local Similarity
Matches 9; Conserv
                                          Similarity
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            Query Match
Best Local 9
                                                                      Matches
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Length 521

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A;Cross-references: UNIPROT: P06811; UNIPARC: UP100001721B1; EMBL:M14554
R;Germann, U.A.; Lerch, K.
Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
A;Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospora C3
A;Feterence number: A29762; MUID:87067412; PMID:247240
A;Accession: A29762
A;Accession: A29762
A;Residues: 379-619
A;Residues: 379-619
A;Residues: 379-619
A;Residues: UNIPARC: UP10000168938; GB:M14554; NID:g168823; PIDN:AAA33590.1; PID:g
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-521 < KUR>
A,Residues: 1-521 < KUR>
A,Cross-references: UNIPROT:Q8U6W1; UNIPARC:UP1000000267E; GB:AE008689; PIDN:AAL45489.1;
A,Experimental source: strain C58 (Dupont)
C,Genetics: Atu4695
A,Gene: Atu4695
A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)
NyAlternate names: urishiol oxidase
NyAlternate names: urishiol oxidase
C.Specias Neurospora crassa
C.Specias: Neurospora crassa laccase. Amino- and A.Reference number: A28523; MUID:88087214; PMID:2961749
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A; Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46;
Pred. No.
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Best Local Similarity 50.09
Matches 7; Conservative
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A; Residues: 1-619 <GER>
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                              A; Status: nucleic acid sequence not shown, translation not shown
A; Status: nucleic acid sequence not shown, translation not shown
A; Molecule type: DNA
A; Cross-references: UNIPARC: UP10000168240; EMBL: U14003; NID:g1263172; PIDN:AAA97194.1; F
A; Experimental source: strain K-12
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: D6524
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-319
A; Cross-references: UNIPARC: UP10000168240; GB: MG1655
C; Genetics:
A; Scherimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: YjhH
C; Superfamily: dihydrodipicolinate synthase
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Appointational protein AGR_L_975GM [imported] - Agrobacterium tumefaciens (strain C58, Cer C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Date: 25-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 233-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell strengt, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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A;Gene: AGR L 975GM
A;Map position: linear chromosome
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hypothetical protein Atu4695 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan_2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
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        Status: nucleic acid sequence not shown; translation not shown: Molecule type: DNA
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Pred. No. 34;
1; Mismatches 6; Indels
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ilarity 50.0%;
Conservative
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Best Local Similarity
المحافظة المح
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-510 < KUR>
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Best Local Similarity
    A; Accession: S56523
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C; Accession: AE2954
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Cikeywords: copper, glycoprotein; oxidoreductase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <NAT>
F;2-49/Domain: propeptide #status predicted <NAT>
F;2-49/Domain: propeptide #status predicted <NAT>
F;316-312/Domain: midlo-terminal beta-barrel #status predicted <BB2>
F;316-312/Domain: midle beta-barrel #status predicted <BB3>
F;319-282,295,340,422,444/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;144,480/Binding site: copper (His) (type 2) #status predicted
F;477,549,554/Binding site: Copper (His) (cype 1) #status predicted
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C;Species: Brucella melitensis
C;Species: Ol. Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3425
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Y; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-619 <GERS.
A,Cross-references: UNIPROT:P10574; UNIPARC:UP1000012E1B2; EMBL:M18334; NID:g168827; PID
C,Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: C90595
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: B28523
R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A;Reference number: A28523; MUID:88087214; PMID:2961749
A;Accession: B28523
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Pred. No. 42;
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Pred. No. 61;
1; Mismatches
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C, Superfamily: isoleucine-tRNA ligase
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66.7%;
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Best Local Similarity 63.6
Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-888 <KUR>
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C;Superfamily: laccase
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Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A,Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A,Reference number: AD3252; PMID:11756688
A,Accession: AG3425
A,Status: Preliminary
A,Molecule type: DNA
A,Residues: 1-350 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells; Karp, P.; Romero, P.; Zhang, S. Science 294, 2117-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "hypothetical protein AGR L_3161 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C; Date: Date: Bigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A; Date Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MuID:21608551; PMID:11743194
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A;Residues: 1-350 «KUR»
A;Cross_references: UNIRROT:Q8UAY2; UNIPARC:UPI00001647C7; GB:AE008689; PIDN:AAL44051.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-370 «KUR»
C;Cross-references: UNIPROT:Q8UAY2; UNIPARC:UPI0000D211E; GB:AE007870; PIDN:AAK90154.1;
C;Genetics:
A;Gene: AGR_L_3161
                                                                                                                                                                                                                             A;Cross-references: UNIPROT:08YFX3; UNIPARC:UPI0000058056; GB:AE008917; PIDN:AAL52570.1; A;Bxperimental source: strain 16M C;Genetics:
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Rocession: AE2954
A,Status: preliminary
A,Nolecule type: DNA
A,Nolecule type: DNA
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Best Local Similarity 47.4.
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Best Local Similarity
Matches 9; Conserva
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A; Map position: linear chromosome
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1; Query Match 39.2%; Score 45.5; DB 2; Length 370; Best Local Similarity 47.4%; Pred. No. 29; Matches 9; Conservative 2; Mismatches 7; Indels 1; Gaps

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Search completed: February 15, 2006, 22:25:22 Job time : 40 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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Duncan M.J.;

Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL, AY046414; AAK94504.1; -; Genomic_DNA.

InterPro; IPR007921; GHAB.

InterPro; IPR0079218; SibA.
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MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Q938VO_1
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
Streptococcus mutans
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=58N3;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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431 AA; 44650 MW; 05D38D8BBC4609F CRC64;
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Q9LCJS AEKPU
Q6ZICZ OKYSA
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Q5KY63 GEOKA
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Q1-DEC-2001 (TrEMBLrel. 19, Cr
Q1-DEC-2001 (TrEMBLrel. 19, La
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Glucan-binding protein B.
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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            GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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STRAIN=3VF4;
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MEDLINE-21153617; PubMed=11254612;
MEDLINE-21128/IAI.69.4.2493-2501.2001;
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
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NUCLEOTIDE SEQUENCE.

STRAIN=28-5;

MEDLINE=21481977; PubMed=11598074;

MEDLINE=21481977; PubMed=115980.701;

DOI=10.1158/IAI.69.11.6987-6998.2001;

Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;

"A 60-Kilodalton immunodominant glycoprotein is essential for cell

"A 60-Kilodalton immunodominant glycoprotein is essential for cell

"A non-integrity and the maintenance of cell shape in Streptococcus

"A continue of cell shape in Streptococcus
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                 clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL, AV046410; AAK945000.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
FRAM; PF05.57; CHAP; 1.
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PROSITE; PR01852; SIBAPROTEIN.
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding I
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Pred. No. 1.8e-09;
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

EMBL, AF338445; AAK08104.1; -; Genomic_DNA.

EMBL, AF338451.1; AR454501.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.
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STRAIN=UALS9 / ATCC 700610 / Serotype c;
STRAIN=UALS9 / ATCC 700610 / Serotype c;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D.J., McShan W.M., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
Perretti J.J.,
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01-MAR-2004 (TrEMBLrel, 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
                                                                                                                                                                                                                                                                                                        MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Name=gppB; OrderedLocusNames=SMU.22;
Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                     Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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44592 MW; 3EBE21FC5E47232E CRC64;
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Pred. No. 1.8e-09;
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100.0%; Pred. No. 1.8e-09;
ive 0; Mismatches 0;
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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PROSITE; PS50911; CHAP; 1.
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PROSITE; PS50911; CHAP; 1.
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QBDWM3;
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Best Local Similarity 100.
Matches 20, Conservative
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                                                                                       NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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SEQUENCE 431 AA;
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NCBI_TaxID=1309;
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Matches

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Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:691-6941(2001).

EMBL; AYO46412; AAK94502.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR00148; SibA.

Figm; PP05257; CHAP: 1.
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"Genome of the bacterium Streptococcus pneumoniae strain R6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 116; DB 2; Length 432; 100.0%; Pred. No. 1.8e-09; ive 0; Mismatches 0; Indels
                        MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=gsp-781; OrderedLocusNames=spr2021;
Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
General stress protein GSP-781.
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EMBL, ABCOGSG6, ALGO823.1; -; Genomic_DNA.

PIR, 998124; B98124.

PIR, 695258; G95258.
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PROSITE; PSS0911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW;
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Best Local Similarity 100.0
....hes 20; Conservative
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QBDMY4;
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Best Local Similarity 78.9
Matches 15; Conservative
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Gaps
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 1.8e-09;
tive 0; Mismatches 0;
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EMBL, AX046413; AAK94503.1; -; Genomic_DNA.

InterPro; IPRO01921; CHAP.

InterPro; IPRO0148; SibA.

Pfam; PF05257; CHAP; 1.

PRINTS; PR04852; SIBAAPROTEIN.

PROSTE; PS50911; CHAP; 1.

SEQUENCE 432 AA; 44652 MW; 3F88ECB9A1F3BE4
0; Mismatches
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                                                                                      403 OEANYAGNOSIGNYRGWFNP 422
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0938V2;
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20; Conservative
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Matches

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RESULT 5
10938VI 7
10938VI

RESULT 6
(93872 ST)
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Gaps

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Length 447;

76.7%; Score 89; DB 2; I 84.2%; Pred. No. 3.1e-05;

1; Mismatches

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1 25 Potential.
26 447 PcsB protein.
447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
EMBL, AJ277292, CAC28144.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                       2 EANYAGNOSIGNYRGWFNP 20
                                                             Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
                                                                                                                                                                                                                                                       Local Similarity 84.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PcsB protein.
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                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                        Query Match
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Q8E7X9 STRA3
ID Q8E7X9 S'
AC Q8E7X9;
DT 01-MAR-2(
                                                                                                                                Signal.
SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8E2H1
      S F F W D R W F F F S
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                                                                                                                                                                                                                                                                                                                                       MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217; MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217; Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple B.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chhatwal G.S.; "Identification and molecular analysis of PcsB, a protein required for "Identification of group B streptococcus."; J. Bacteriol. 183:1175-1183(2001).
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MEDLINE=21101799; PubMed=11157929;
DOI=10.1128/JB.183.4.1175-1183.2001;
Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
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78.9%; Pred. No. 2.1e-06;
live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                        Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 AA; 41697 MW; BSASA860FAEA77DD CRC64;
                                                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                      392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007509; AAK76264.1; -; Genomic_DNA.
PIR; B98124; B98124.
PIR; G95258; G95258.
                                                                      PRT;
                                                                                                              Created)
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InterPro; IPR001921; CHAP.
InterPro; IPR00148; SibA.
Pfam; PP05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS0911; CHAP; 1.
Complete 2392 AA; 41697 MW;
                                                                                                          01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 293:498-506(2001).
                                                                                                                                                                          Secreted 45 kd protein.
OrderedLocusNames=SP2216;
                                                                    Q97N55_STRPN PRELIMINARY;
Q97N55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9AKA4 STRAG PRELIMINARY;
Q9AKA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                        Streptococcus pneumoniae.
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Best Local Similarity
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09AKA4_STRAG
1D 09AKA4_STRAG
DT 01-JUN-20
DT 01-JUN-20
DE PCSB prot
GN Name=pcse
GN STRAIN=GN
KN [1]
RP NUCLEOTII
RP NUCLEOTII
RP NUCLEOTII
RP NUCLEOTII
RP NUCLEOTII
RP ACHAIN=GN
RP CHAIN=GN
RP CHAIN
RP CHAIN=GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002). EMBL; ARD14192; AAM98925.1; -; Genomic_DNA. TIGR; SAG0017; -. InterPro; IPR007921; CHAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.7%; Score 89; DB 2; Length 447
84.2%; Pred. No. 3.1e-05; Indels
                                                                                                                                                                                                                                                                                                                                        Name=pscB; OrderedLocusNames=SAG0017;
Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
GEOTIENCE 447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 AA.
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                                                                                                                                                                 PRT;
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2 EANYAGNOSIGNYRGWFNP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro; IPR009148; SibA.
                                                                                                                                                        QBE2H1_STRAS PRELIMINARY;
QBE2H1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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nes 16; Conservó
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169 AA; 18390 MW; 8A1653A8B5B8B769 CRC64;
                                                                                                                                                            2 EANYAGNOSIGNYRGWFNP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sagalist; gbs1805; -.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
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OrderedLocusNames=str0443;
                                                                                                                                                                                                                                                                                                                    QBE3F4_STRA3 PRELIMINARY;
Q8E3F4;
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QSM137;
                                                                                                               14; Conservative
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STRAIN=NEM316 / Serc
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                                                                    Query Match
Best Local Similarity
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NCBI_TaxID=299768;
    Complete proteome.
SEQUENCE 169 AA;
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SEQUENCE 169 AA
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OSM137 STR
ID OFM STR
ID OLFE
DT 01-FE
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                                                                                                                                                                                                                            STRAIN=NEM116 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Streptococcus agalactiae, a pathogen causing
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                                                                                          Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein SAG1762.
OrderedLocusNames=SAG1762;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AA
                                                                                                                                                                                                                                                                                                                                                                 invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766843; CAD45661.1; -; Genomic_DNA.
                                             PcsB protein.
Name=pcsB; OrderedLocusNames=gbs0016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 ESNYAGNMSIGNYRGSFNP 435
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InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; I.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sagalist; gbs0016; -.
InterPro; IPR007921; CHAP.
InterPro; IPR001448; SibA.
Pfam; PP05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBDXT4_STRAS PRELIMINARY;
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                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 16; Conserv
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NCBI_TaxID=216466;
                                                                                                                                                       NCBI_TaxID=216495;
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MEDLINE=222424508; WebMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Maadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                          Gaps
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PubMed=15543131; DOI=10.1038/nbt1034;
Bolottin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Golteman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.4%; Score 84; DB 2; Length 169; 73.7%; Pred. No. 6.4e-05; ive 3; Mismatches 2; Indels
                 Score 84; DB 2; Length 169;
Pred. No. 6.4e-05;
3; Mismatches 2; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
72.4%; Sco...
73.7%; Pred. No. o...
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Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766853; CAD47464.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last seqn 01-MAR-2004 (TrEMBLrel. 26, Last annothypothetical protein gbs1805. OrderedLocusNames=gbs1805;
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Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P., Decaris B., Leblond-Bourget N.;

Decaris B., Leblond-Bourget N.;

Lose, a Chimmeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";

J. Bacteriol. 187:273-2746(2005).

SEMBL, AY65844; AAN3369.1; -; Genomic DNA.

SEQUENCE 461 AA; 48498 MW; CA72A95F945BD7A4 CRC64;
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Angui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
Gomplete sequence and comparative genome analysis of the dairy
acceptate sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
Rami. CP000024; AAV62043.1; -; Genomic_DNA.
Rami. CP000124; AAV62043.1; -; Genomic_DNA.
Rami. PF05257; CHAP; 1.
Ream, PF05257; CHAP; 1.
Ream, PF05257; CHAP; 1.
Ream, PF05257; CHAP; 1.
Complete protecome.
SQUENCE 129 AA; 13136 MW; 7ADBD47F41B7D4B3 CRC64;
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Best Local Similarity 73.7%; Pred. No. 0.00029;
Matches 14; Conservative 2; Mismatches 3; Indels
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI_TaxID=1308;
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Q56SA7 STRTR PRELIMINARY; PRT; 461 AA.

LO G56SA7;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence or Streptococcus.
OS Streptococcus.
ON NCBI_TAXID=1308;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA BOTGSE F., Layec S., Thibessard A., Fernandez A., Gintz RA Borges F., Lablond-Bourget N.;
RA BOTGSE F., Lablond-Bourget N.;
RA BOTGSE F., Lablond-Bourget N.;
RI "CSE, a Chimeric and Variable Gene, Encodes an Extracel RT Involved in Cellular Segregation in Streptococcus therm R. J. Bacteriol. 187:2737-2746 (2005).
DR EMBL; AY695844; AAW33692.1; -; Genomic_DNA.
SQ SEQUENCE 461 AA; 48498 MW; CA72A95F945BD7A4 CRC64;
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Search completed: February 15, 2006, 22:24:38 Job time : 230 secs

429 ESNYAGNMLIGNYRGTFDP 447

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LENGTH: 20
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Sequence 23, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 320, Appl
Sequence 12794, Appl
Sequence 12794, Appl
Sequence 12794, Appl
Sequence 106017, Sequence 106017, Sequence 106017, Sequence 106017, Sequence 106017, Sequence 107, Appl
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                                                                                      February 15, 2006, 22:36:04; Search time 165 Seconds (without alignments) 50.646 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-383-930-29
US-10-383-930-39
US-10-383-930-39
US-10-383-930-39
US-10-797-821-29
US-10-797-821-29
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US-10-47-792-600
US-10-47-792-600
US-10-425-115-325660
US-10-425-115-325660
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US-10-425-115-325600
US-10-425-115-32311
US-10-43-1024-107
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US-10-43-1024-107
US-10-450-763-55253
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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US-10-797-821-22

Sequence 22, Application US/10797821

Sequence 22, Application US/10797821

Sequence 22, Application WIS20050031633A1

Sequence 22, Application No. US20050031633A1

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 2569-020

CURRENT APPLICATION NUMBER: US/10/797,821

PRIOR PLILING DATE: 2004-03-09

PRIOR PLILING DATE: 2003-03-07

PRIOR PLILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR PLILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 09/290,049
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 18914, A
32852, A
23683, A
43119, A
1912, Ap
55252, Ap
712, App
40380, A
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16, Appl
57, Appl
14, Appl
9, Appli
56, Appli
14, Appl
134, Appl
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US-10-22
US-10-383-930-22
Sequence 22, Application US/10383930
Publication No. US20040127400A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/402,483
FRIOR FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
SRIOR FILING DATE: 2002-08-08
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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        US-10-029-386-32852
US-10-029-493-23683
US-10-369-493-23683
US-10-094-742-13119
US-10-094-742-13119
US-10-112-94-712
US-10-112-94-712
US-10-152-548-16
US-10-152-548-16
US-09-847-102A-57
US-10-152-548-16
US-10-152-548-16
US-10-131-74-14
US-10-382-586A-9
US-10-301-74-14
US-10-201-74-14
US-10-201-74-14
US-10-201-74-14
US-10-201-74-14
US-10-201-74-14
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100.0%; Pred. No. 4.4e-10;
iive 0; Mismatches 0;
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; ORGANISM: Streptococcus mutans
US-10-383-930-22
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-383-930-30
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| Sequence 30, Application US/10383930
| Sequence 30, Application US/10383930
| Publication No. US20040127400A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Taubman, Martin A
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
| FILE REPERENCE: 25669-018
| CURRENT APPLICATION NUMBER: US/10/383,930
| PRIOR APPLICATION NUMBER: 60/402,483
| PRIOR PILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-03-07
| RIGHT FOR FILING DATE: 2002-03-07
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: PatentIn version 3.2
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GENERAL INFORMATION:

APPLICANT: Smitch, Daniel J

APPLICANT: Smitch, Daniel J

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REPERENCE: 25669-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT FILING DATE: 2003-03-07

PRIOR PILING DATE: 2002-08-08

SPRIOR PILING DATE: 2002-08-07

SPRIOR PILING DATE: 2002-08-07

SOFTWARE: Petentin vergion 3.2

SEQ ID NOS: 41
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Pred. No. 8.7e-09;
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100.0%; Score 116; D
Best Local Similarity 100.0%; Pred. No. 8.7
Matches 20; Conservative 0; Mismatches
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-04-13
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
LENGTH: 20
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                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: GbpB peptide
US-10-797-821-22
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; ORGANISM: Streptococcus mutans
US-10-383-930-29
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Sequence 29, Application US/10797821

Sequence 29, Application US/10797821

Publication No. US20050031633A1

GENERAL INPORMATION:

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 2569-020

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 1909-04-12

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PLING DATE: 1999-04-12

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR PLING DATE: 1999-04-12

PRIOR PLING DATE: 1999-04-13

PRIOR PLING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Version 3.2

SEQ ID NO 29
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APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTENCY: Taubman, Martin A
FILE REPERENCE: 2566 9.018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT PILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-08-08
PRIOR PELING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SCOFTWARE: Patentin Version 3.2
SEQ ID NO 33
LENGTH: 431
                                                                                                                                  Query match 100.0%; Score 116; DB 4; Length 431; Best Local Similarity 100.0%; Pred. No. 8.7e-09; Matches 20; Conservative 0; Mismatches n. Tulal-
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Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 33, Application US/10383930; Publication No. US20040127400A1; GENERAL INFORMATION:
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SEQ ID NO 30
LENGTH: 431
TYPE: PRT
ORGANISM: Streptococcus mutans
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 20; Conserv
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LENGTH: 432
TYPE: PRT
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GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR PELING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 45

SEQ ID NOS: 45

SEQ ID NOS: 45
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Fublication No. US20050031633A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens
TITLE OF INVENTION WIGHER: US/10/797,821
CURRENT PILING DATE: 2004-03-09
CURRENT FILING DATE: 2004-03-09
FRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR PAPLICATION NUMBER: 60/402,483
PRIOR PAPLICATION NUMBER: 60/402,483
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-03-07
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PRIOR FILING DATE: 2002-03-07
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100.0%; Score 116; DB 5; Length 431;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                               403 QEANYAGNQSIGNYRGWFNP 422
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; Sequence 30, Application US/10797821
; Publication No. US20050031633A1
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; LENGTH: 431
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
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; ORGANISM: Streptococcus mutans
US-10-797-821-30
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APPLICANT: Taubman, Martin A
ITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 2566-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 116; DB 4; Length 432; 1 Similarity 100.0%; Pred. No. 8.7e-09; 20; Conservative 0; Mismateria.
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                               US-10-383-930-31
; Sequence 31, Application US/10383930
; Publication No. US20040127400A1
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RESULT 13
US-10-472-928-4652
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US-10-617-320-3230
                                                                             TYPE: PRT
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Sequence 32, Application US/1079821

Publication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT APPLICATION NUMBER: 10/383,930

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR FILING DATE: 2003-03-07

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-09-04

PRIOR FILING DATE: 1999-04-12

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR FILING DATE: 1999-04-12
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                                      100.0%; Score 116; DB 4; Length 432; 100.0%; Pred. No. 8.7e-09;
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; Pred. No. 8.7e-09;
0; Mismatches 0;
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CRGANISM: Streptococcus mutans
US-10-797-821-31
; ORGANISM: Streptococcus mutans US-10-383-930-32
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                 Best Local Similarity 100.
Matches 20; Conservative
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US-10-797-821-31
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Publication No. US20050136404A1

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE

THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHIRON SpA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: PO26926W0
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT PILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: Seqwing9, version 1.03
SEQ ID NO 4652
                                                                                                                                                                                                                                                                                                                            Gaps
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OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15904062 (0.E+01)
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4652, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 432
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CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Streptococcus pneumoniae
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COUNTRY: USA
                                                                                                                                                                                       ; ORGANISM: Streptococcus mutans
US-10-797-821-32
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Matches 15, Conservative
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Search completed: February 15, 2006, 22:39:15 Job time : 166 secs
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US-10-474-792-600
; Sequence 600, Application US/10474792
; Publication No. US200400236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Agureky, Robert
; APPLICANT: Mickbarg, Elliot
; APPLICANT: Wickbarg, Elliot
; APPLICANT: Wickbarg, SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REPERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SEQ ID NO 600
; SEQ ID NO 600
; LEMETH: 398
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           CURRENT APPLICATION DATA:

SOFTWARE: «Unknown:

APPLICATION UNMERE: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
REGISTRATION NUMBER: 40,489
REFERRENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEFAX: (781)893-5077
INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TTYPE: amino acids
TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
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Sequence 22. Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdew.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT FILING DATE: 2005-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Streptoccoccus mutans UA159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 QEANYAGNQSIGNYRGWFNP 422
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Best Local Similarity
Matches 20; Conserv
RESULT 2
US-11-052-554A-252
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Query Match
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Sequence 252, App
Sequence 352, App
Sequence 314, App
Sequence 153, App
Sequence 153, App
Sequence 153, App
Sequence 34, Appl
Sequence 39, Appl
Sequence 139, Appl
Sequence 142, Appl
Sequence 143, Appl
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Sequence 388, App
Sequence 173, App
Sequence 179, App
Sequence 5, Appli
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Sequence 14, Appl
Sequence 3, Appli
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
          GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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US-11-052-554A-358
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US-11-062-554A-358
US-11-080-386-214
US-11-080-386-214
US-11-080-386-314
US-11-188-505-34
US-11-188-505-34
US-11-171-257-39
US-11-170-653-27
US-11-052-554A-133
US-11-052-554A-133
US-11-052-554A-133
US-11-064-377-388
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Maximum Match 100%
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Match Length
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Perfect score:
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Squence 210, Application US/11052554A

Squence 210, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2004-07-07

PRIOR FILING DATE: 2004-07-07

PRIOR FILING DATE: 2004-07-07

PRIOR FILING DATE: 2004-07-07

PRIOR FILING DATE: 2004-07-07

NUMBER OF SEQ ID NOS: 763

SOFTWARRE PATCHINI VERSION 3:3

SOFTWARE PATCHINI VERSION 3:3
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1523, Appli
1360, Ap
11315, Appl
151, Appl
151, Appl
110, Appl
110, Appl
1121, Appl
121, Appl
15, Appl
16, Appl
17, Appl
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US-11-106-820-3

US-11-143-077-3

US-11-190-364-3

US-11-096-464-5

US-11-054-515-1363

US-11-084-515-1363

US-11-084-686-11315

US-11-07-877-878-151

US-11-07-673-38

US-11-052-554A-130

US-11-052-554A-130

US-11-052-554A-130

US-11-062-554A-130

US-11-062-554A-130

US-11-062-554A-130

US-11-061-848-35

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US-11-061-848-12
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Sequence 390, Application US/11004590

Sequence 390, Application US/11004590

Publication No. US2006000883A1

GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan

APPLICANT: Desiarias, John R.

APPLICANT: Hammond, Phillip W.

TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF

CURRENT APPLICATION NUMBER: US/11/004,590

CURRENT APPLICATION NUMBER: US 60/527,167

PRIOR PILING DATE: 2004-10-14

PRIOR APPLICATION NUMBER: US 60/619,665

PRIOR FILING DATE: 2004-06-13

PRIOR FILING DATE: 2004-10-14

NUMBER OF SEQ ID NOS: 458

SOFTWARE: PatentIn version 3.3

SOFTWARE: PatentIn version 3.3
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Indels
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                                                                                                                                          US-10-510-386-214

| Sequence 214, Application US/10510386
| Publication No. US20050244922A1
| GENERAL INFORMATION:
| APPLICANT: Andersen, Jens Tonne
| APPLICANT: Clausen, Ib Groth
| APPLICANT: Clausen, Steen Troels
| APPLICANT: Olsen, Peter Blarke
| APPLICANT: Rasmussen, Michael Dolberg
| TITLE OF INVENTION: Improved Bacillus Host
| FILE REFERENCE: 10294.204-US
| CURRENT APPLICATION NUMBER: US/10/510,386
| CURRENT FILING DATE: 2004-10-04
| NUMBER OF SEQ ID NOS: 248
| SEQ ID NO 214
| LENGTH: 702
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Pred. No. 9.1;
3; Mismatches
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3; Mismatches
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Pred. No.
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                                                                                    178 ESNYKDQQWVDNYRGWFDP 196
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                                           2 EANYAGNQSIGNYRGWFNP 20
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Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
11; Conservative
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Sequence 358, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR PILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION WUMBER: US/11/052,554A
CURRENT PEPLING DATE: 2005-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: APPLICATION WOMBER: 13
SOFTWARE: Astentin version 3.3
LENGTH: 211
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                                                                                                                                                        Length 398;
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60.0%; Pred. No. 0.00068;
Live 3; Mismatches 5;
                                                                                                                                                    Score 77; DB 7; I
Pred. No. 0.00018;
4; Mismatches 3;
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 252
; LENGTH: 398
; TYPE: PRT
US-11-052-554A-252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptococcus mutans UA159
US-11-052-554A-352
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                                                                                                                                                      Query Match
Best Local Similarity 63.2%;
Matches 12; Conservative
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Matches 12; Conservative
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Best Local Similarity
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LENGTH: 544
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APPLICANT: NATORIAN DOUGLAS J
APPLICANT: RAO, PATRICIA
APPLICANT: RAO, PATRICIA
APPLICANT: RAO, PATRICIA
APPLICANT: RAO, PATRICIA
TITLE OF INVENTION: INDUCTION IN PRIMATES
TITLE OF INVENTION: INDUCTION IN PRIMATES
TITLE OF INVENTION: 1005: 06-21
CURRENT APPLICATION NUMBER: US/11/158,505
CURRENT FILICA DATE: 2005-06-21
PRIOR APPLICATION NUMBER: 60/582,181
PRIOR PLING DATE: 2004-06-22
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATENTIN VET: 3.3
LENGTH: 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Humanized CD8 CTHER INFORMATION: antibody light chain construct US-11-158-505-34
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Pred. No. 93;
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100.0%; Pred. No. >c,
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APPLICANT: Biosynexus Incorporated
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PatentIN version 3.1
SEQ ID NO 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-485-517-355

'Sequence 355, Application US/10485517

'Publication No. US20050256299A1

'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/10771257; Publication No. US20050288864A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus US-10-485-517-355
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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nes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 YRGWFN 19
GENERAL INFORMATION:
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US-10-771-257-39
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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; Publication No. US20050260212A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhang, Yongke
; APPLICANT: Law, Debbie
TITLE OF INVENTION: ANTI-LFL2 ANTIBODIES FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT;
TITLE OF INVENTION: OF CANCER
FILE REFERENCE: 05882.023. NPUS02
CURRENT APPLICATION NUMBER: US/11/089,872
CURRENT APPLICATION NUMBER: 60/557,440
PRIOR PILING DATE: 2004-03-26
PRIOR PILING DATE: 2004-03-26
PRIOR FILING DATE: 2004-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHLIN Version 3.2
SETWARE: PATCHLIN Version 3.2
                                                                                               Sequence 153, Application US/11052554A

Sequence 153, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:

APPLICATUS

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THE 2005-02-07

CURRENT PILING DATE: 2005-02-07

PRIOR PILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SEQ ID NOS: 763

SEQ ID NOS: 763

SEQ ID NOS: 763
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36.2%; Score 42; DB 7; Length 987;
Best Local Similarity 42.9%; Pred. No. 82;
Matches 9; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.3%; Score 41; DB 7; Length 138; Best Local Similarity 85.7%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-153
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; Publication No. US20060002921A1
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SONINNYLGWY 36
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TYPE: PRT
ORGANISM: Mus musculus
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US-11-158-505-34
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us-10-797-821-22.rapbn

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2; Mismatches
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34.1%; Score 39.5; 1
Best Local Similarity 41.7%; Pred. No. 46;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: H. insolens
US-11-170-653-27
RESULT 13
US-11-052-554A-142
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US-11-052-554A-133
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US-11-170-653-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Derived protein sequence of scFv US-11-127-677-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 Application US/11127677

Publication No. US20050272107A1

GENERAL INFORMATION:

APPLICANT: Medical Research Council

APPLICANT: Tanaka, Tomoyuki

TILE OF INVENTION: Intracellular antibodies

FILE REFERENCE: 18396/2462

CURRENT APPLICATION NUMBER: US/11/127,677

CURRENT APPLICATION NUMBER: COS-12

FRIOR FILING DATE: 2005-05-12

PRIOR FILING DATE: 2005-11-14

PRIOR FILING DATE: 2002-11-15

PRIOR FILING DATE: 2002-11-15

SEQ ID NOS: 150

SOFTWARE: PatentIn version 3.1

LENGTH: 108
             APPLICANT: Calculated, Amos
APPLICANT: Maritan, Amos
APPLICANT: Wisintin, Michela
APPLICANT: Rabbitts, Terrence H
APPLICANT: Settanni, Giovanni
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 1836/2272
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: CG/GB02/03512
PRIOR APPLICATION NUMBER: PCT/GB02/03512
PRIOR APPLICATION NUMBER: GB 0119004.0
PRIOR APPLICATION NUMBER: GB 011577.1
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NOS: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 6
Pred. No. 18;
3; Mismatches
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54.5%;
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ORGANISM: Artificial sequence
         Cattaneo, Antonino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.5
Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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26 SQSIGSYLNWY 36
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US-10-771-257-39
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Sequence 142, Application US/11052554A

Sequence 142, Application US/11052554A

Publication No. US20050288866A1

GENERAL INPORMATION:
APPLICANI Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE PATCHIN VERSION 3.3

SOFTWARE PATCHIN VERSION 3.3
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Sequence 27 Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:
APPLICANT: Danisoco A/S

APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
ITILE OF INTENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitors
ITILE OF PRIOR PAPLICATION NUMBER: US/11/170,653
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/237,386
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 
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34.1%; Score 39.5; DB 7; Length 3300;
Best Local Similarity 43.5%; Pred. No. 6.4e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 7; Gaps
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GENERAL INFORMATION:
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GenCore version 5.1.7
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- protein search, using sw model OM protein

February 15, 2006, 17:57:02; Search time 113.754 Seconds (without alignments) 1668.609 Million cell updates/sec Run on:

US-10-797-821-31 2110 Title: Perfect score:

1 MKKRILSAVLVSGVTLSSAT......SIGNYRGWFNPGSVSYIYPN 432 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

2443163 Total number of hits satisfying chosen parameters:

2443163 seqs, 439378781 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 21:\* 1: genesermino Database :

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Add93651 Streptoco	Adx37274 Streptoco	Add93652 Streptoco	Adx37275 Streptoco	Add93650 Streptoco	Adx37273 Streptoco	Add93649 Streptoco	Adx37272 Streptoco	Aeb91500 Microbial	Add93653 Streptoco	Adx37276 Streptoco	Abp29684 Streptoco			Adv81808 Streptoco	Adv79645 Streptoco	Aeb91542 Microbial	Abp25919 Streptoco	Adr83884 S. pyogen	Abp25918 Streptoco	ß	Adt50226 S pneumon	Adt50165 S_pneumon	Adr94595 Novel S.
SUMMAKIES	ID	ADD93651	ADX37274	ADD93652	ADX37275	ADD93650	ADX37273	ADD93649	ADX37272	AEB91500	ADD93653	ADX37276	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645	AEB91542	ABP25919	ADR83884	ABP25918	ABU02747	ADT50226	ADT50165	ADR94595
	DB	7	σ	7	σ	7	σ	7	σ	σ	7	σ	Ŋ	œ	æ	8	œ	σ	ស	80	'n	9	œ	œ	œ
	ð Query Match Length DB	432	432	432	432	431	431	431	431	431	431	431	447	447	447	447	447	398	398	398	395	392	392	392	399
d	Query Match	100.0	100.0	99.5	99.2	98.7	98.7	98.6	98.6	98.6	98.4	98.4	58.5	58.5	58.5	58.5	58.5	51.8	51.5	51.5	51.1	50.2	50.2	50.2	50.2
	Score	2110	2110	2099	2099	2083.5	2083.5	2079.5	2079.5	2079.5	2075.5	2075.5	1234.5	1234.5	1234.5	1234.5	1234.5	1093	1087	1087	1077.5	1059	1059	1059	1059
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Aea58465	Adk47859	Adt50227	Aar14150	Aar14530	Abb55584	Abu29734	Adc95468	Aay22579	Adv16553	Adh88105	Aay00250	Abp43469	Abu88497	Abu13748	Adv16734	Ady39216	Adh87829	Aay00251	Abp43470	Abu88498	
AEA58465	ADK47859	ADT50227	AAR14150	AAR14530	ABB55584	ABU29734	ADC95468	AAY22579	ADV16553	ADH88105	AAY00250	ABP43469	ABU88497	ABU13748	ADV16734	ADY39216	ADH87829	AAY00251	ABP43470	ABU88498	
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399	392	392	461	461	456	524	525	210	482	497	449	449	449	449	449	449	450	422	422	422	
50.2	50.1	50.1	32.3	32.3	31.3	27.9	27.7	26.6	25.1	25.1	23.7	23.7	23.7	23.7	23.7	23.7	23.7	21.4	21.4	21.4	
1059	1058	1058	681.5	680.5	099	588.5	584.5	561	529	529	500.5	500.5	500.5	500.5	500.5	500.5	500.5	452.5	452.5	452.5	
52	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B. ADD93651 standard; protein; 432 AA. (first entry) 29-JAN-2004 ADD93651; RESULT 1 ADD93651 

Streptococcus mutans.

WO2003075845-A2.

18-SEP-2003.

07-MAR-2003; 2003WO-US006962.

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

WPI; 2003-845091/78. GENBANK; AY046412. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 5; Page 8; 49pp; English.

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in

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Streptococcus mutans.
      2005-151644/16
                                                                                                                                      Sequence 432 AA;
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                                                                                               QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
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                                               Gaps
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microparticle; major histocompatibility complex; tooth disease.
                                432;
                                Length
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus mutant glucan binding protein B variant
                             Score 2110; DB 7;
Pred. No. 5.9e-134;
Mismatches 0;
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402433P.
07-MAR-2003; 2003US-00383930.
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100.0%;
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passive immunisation
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(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                      ADX37274 standard;
                                       Local Similarity
                Sequence 432 AA
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New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                            The invention relates to a composition comprising a fragment of a gl binding protein-B (GbpB) and a biocompatible microparticle, where th fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds Streptococcus mutans GbpB protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2110; DB 9;
100.0%; Pred. No. 5.9e-134;
ive 0; Mismatches 0;
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                                                                                                                                       3; SEQ ID NO 31; 73pp; English
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Matches 432; Conservative
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or mutriepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
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                                                                                                                                                                                                       composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatiblity complex class II protein.
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                                                                                                                                                                                                                                                                                          5; Page 8; 49pp; English
                07-MAR-2003; 2003WO-US006962
                                                07-MAR-2002; 2002US-0363209P
08-AUG-2002; 2002US-0402483P
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Matches 429; Conservative
                                                                                                                                    Taubman MA;
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241 KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
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                                                                                                                     immunogenicity; immune stimulation; glucan binding protein-B; nicroparticle; major histocompatibility complex; tooth disease
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                                                                                         Streptococcus mutant glucan binding protein B variant #4
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ADX37275 standard; protein; 432
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
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TAUBMAN M A.
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nes 429; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                          Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
           SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                ASAAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
                                                             Length 431;
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Pred. No. 3.6e-132;
2; Mismatches 1;
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                                                                                                                                                                                         ADD93650 standard; protein; 431
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99.1%;
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                                                                                                                                      TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA
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KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
                                                                                                           TIAONTNALNTOQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAAAAA
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microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADX37273 standard; protein; 431 AA.
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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TAUBMAN M A.
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Best Local Similarity 99.1 Matches 428; Conservative

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MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG

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"HLA-binding peptide"
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08-AUG-2002; 2002US-0402483P.
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Best Local Similarity 98.8
Matches 427; Conservative
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protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds Streptococcus mutans GbpB protein of the invention.
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                                                    Length 431;
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (WHC) caries. The compositions comprise major histocompatibilty complex (WHC) covalently linked with peptides sepecially HLA-binding peptides, compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
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Pred. No. 6.7e-132;
                                                               "HLA-binding peptide"
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fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                        Score 2079.5; DB 9; Length 431;
Pred. No. 6.7e-132;
2; Mismatches 2; Indels 1;
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20-JUL-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the
                                                                                          INAIINSKSVSDAINRVSAIREVVSANEKALQQQEQDKAAVEQKQQENQAAINTVAANQE
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                                  tiaontnalntooaoleaaolnloaelttaodokativaokaaaebaaroaaaaba
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microparticle; major histocompatibility complex; tooth disease.
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0402483P.
07-MAR-2003; 2003US-0402483P.
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(TAUB/) TAUBMAN M A.
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                                                           algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer; gastrointestinal-gen.; urinary tract infection; antimicrobial;
Microbial pathogen adhesin protein sequence, SEQ ID NO:210.
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ADD93653

The present invention relates to a computational method (MI) for identifying adhesin and adhesin-like proteins, by computing the sequencebased attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (Pad) as encoding adhesin and adhesin-like proteins, having 274 fully defined 162-1151 base pair (SEQ ID NO: 38-658) sequences; a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having 105 fully defined 162-1151 base pairs (SEQ ID NO: 659-763); a set of 279 annotated adhesin and adhesin-like proteins, having 105 fully defined 53-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (MI). (MI) is useful for identifying adhesin and adhesin-like proteins, of therapeutic potential, and identifying and short-listing proteins for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms. (MI) is discovery and preventing therapeutics for whooling cough, pneumonia, gastric ulcer and urinary tract infections. (M.) identifies adhesins from faitently related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M.) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network. useful for identifying putative adhesins that are important in drug Claim 16; SEQ ID NO 210; 402pp; English 

Sequence 431 AA;

240 61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120 61 OVSALOTOQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120 121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQGENQAAINTVAANQE 180 121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQGGDKAAVEQKQQENQAAINTVAANQE 180 240 KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300 241 KAAAEAKALQEQAAQAQAAA-NNNTQATDVSDQQAAAADNTQAAQTGDSTEQSAAQAVNN 299 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA 360 300 SDQESTTATEAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA 359 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW 420 360 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW 419 9 9 181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVVTIQG TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG Gaps , H Score 2079.5; DB 9; Length 431; Pred. No. 6.7e-132; 2; Mismatches 2; Indels 1; 98.6%; FNPGSVSYIYPN 432 Matches 427; Conservative Best Local Similarity 241 421 181 301 361 Query Match ઠ g ઠે 셤 ò g ò 셤 ઠે g 8 D. ሯ a ò

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B ADD93653 standard; protein; 431 AA. Claim 5; Page 8-9; 49pp; English 07-MAR-2002; 2002US-0363209P. 08-AUG-2002; 2002US-0402483P. 07-MAR-2003; 2003WO-US006962 Smith DJ, Taubman MA; (FORS-) FORSYTH INST. Streptococcus mutans WPI; 2003-845091/78. GENBANK; AY046414. 29-JAN-2004 18-SEP-2003 ADD93653; 

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 5SM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibity complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Dispitopic or multipitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.

1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG ï 7; Length 431; Indels Score 2075.5; DB 7; Pred. No. 1.2e-131; 2; Mismatches 3; 98.4%; Query Match
Best Local Similarity 98.6
Matches 426; Conservative 8

Sequence 431 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
               KAAAEAKALQEQAAQAQAAA -NNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNN
                                                               SDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGGWA
                                                                                                        KAAAEAKALOEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
                                                SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                             ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
                                                                                                                                                                                                                                                                                                                 immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                              Streptococcus mutant glucan binding protein B variant #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2075.5; DB 9;
Pred. No. 1.2e-131;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 33; 73pp; English.
                                                                                                                                                                                                                          protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammals against dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JJN-1999; 99US-0115142P.
12-APR-1999; 99US-0029049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-046483P.
07-MAR-2003; 2003US-00383930.
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Best Local Similarity 98.6%;
Matches 426; Conservative
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                                                                                                                                                      Taubman MA;
                                                                                                                                           FNPGSVSYIYPN
                                                                                                                                                                                                                                                                                                                                                      Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
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Best Local Similarity
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1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG

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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                              INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEÇKQQENQAAINTVAANQE
                                                                                                                                                                                                  SDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                                                                                                                                                                            ASAAAAAYWGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
                 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE
                                                                                                                       TIAONTNALNTOOAOLEAAOLNLOAELTTAODOKATLVAOKAAAEEAAROAAAAAAAEA
                                                                                                                                                  181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAA
                                                                                                                                                                                    KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
                                                                                                                                                                                                                                               SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                                                                                                                                                         ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 AA
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2000GB-00028727.
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07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP29684 standard; protein;
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(GENO-) INST GENOMIC RES.
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streptococcus/GBS (Streptococcus agalactise) or group A streptococcus/GAS (Streptococcus/GBS (Streptococcus/GBS) comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71256 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactise and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bilogical sample. (I) is used to detecramine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins
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QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                                                                         121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
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                                                                                                                                                                                                                                                                                         KAAAEAKALQEQAAQAQAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
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                                                                          1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                  45;
 DB 5; Length 447;
                            98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 GV-QGGQIQVQEANYAGNQSIGNYRGWFNP---GSVSYIYPN 432
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58.5%; Score 1234.5; DB 59.7%; Pred. No. 6.7e-75;
                            43; Mismatches
                            Matches 276; Conservative
              Best Local Similarity
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immune stimulation; antigen; bacterial surface display; hyperimmune serum reactive antigen; vaccine; bacterial infection; antibacterial; infection.
                                                                                                  S agalactiae hyperimmune serum reactive antigen seqid 219
                         ADU69524 standard; protein; 447 AA
                                                                          10-FEB-2005 (first entry)
                                                                                                                                                                          Streptococcus agalactiae.
                                                 ADU69524;
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At the invention describes an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment. Also described are: a hyperimmune serum reactive antigen comprising the vector comprising the nucleic acid molecule, a host cell comprising the vector; a hyperimmune serum-reactive antigen as sequence encoded by the nucleic acid molecule and consisting of e.g., 85, 299, 467 or 812 amino acids; fragments of hyperimmune serum-reactive antigens a process for producing a Streptococcus agalactiae hyperimmune serum consisting, especially a vaccine, comprising the hyperimmune serum composition, especially a vaccine, comprising the hyperimmune serum control acid molecule; an antibody that binds at least to a selective part of the hyperimmune serum-reactive antigen; a hyperimmune serum-reactive antigen; a method for identifying an antibody; a method for identifying an antibody; a method for identifying an antipody; and the hyperimmune serum-reactive antigen to its interaction activity of a hyperimmune serum-reactive antigen to its interaction activity of a hyperimmune serum-reactive antigen to its interaction partner; a process for in vitro diagnosing a disease related to expression of the hyperimmune serum-reactive antigen is useful for isolating, purifying and/or identifying an interaction partner of the hyperimmune serum reactive antigen is useful for isolating, purifying and/or identifying an interaction partner of the hyperimmune serum reactive antigen is useful for isolating is useful for generating a peptide comparising anticalines or for the manufacture of a hyperimmune serum reactive antigen, and and or interaction partner of the hyperimmune serum reactive antigen or is selective. The peptide comparising anticalines or for the manufacture of a hyperimmune serum reactive antigen or is an an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 functional nucleic acid comprising aptamers or spiegelmers. The nucleic acid molecule is useful for the manufacture of a functional ribonucleic acid comprising ribozymes, antisense nucleic acids or siRNA. The nucleic acid molecule, hyperimmune serum-reactive antigen or antibody is useful for the manufacture of a vaccine against S. agalactiae infection. This is
                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule encoding a hyperimmune serum reactive antigen, useful for the manufacture of a vaccine against Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequence of a Streptococcus agalactiae hyperimmune serum
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                                                                                                                                                                                                                                                                           Kallenda S,
                                                                                                                                                                                                                                                                           Horky M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; SEQ ID NO 219; 221pp; English
                                                                                                                                                                                                                                                                         Hanner M,
                                                                                               06-MAY-2004; 2004WO-EP004856
                                                                                                                                               07-MAY-2003; 2003EP-00450112
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276; Conservative
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                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                     QCTWGVKSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVW--NDGGYGHVAYVT 394
                                                                                                                                                                                                                                                                                                                                                                                                    405
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  INTILNSKSVSDAVNRVVAIREVVSANEKMLAQQEADKAALEAKQIENQNAINTVAANKQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                                                                AIENNKAALATQRAQLEAAQLELSAQLTTVQNEKASLIQAKAQAEBAARKAABAQAAABA
                                                                                                                                                                                                                                                     -- VAANTSSANTYPAG
                                                                                                                                                                                                                                                                                  TIAONTNALNTOQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAT
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Poyart C, Trieu CP, Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVANNSSIQVMESNYAGNMSIGNYRGSFNPSASGSVYXIYPN 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GV-OGGOIQVQEANYAGNQSIGNYRGWFNP---GSVSYIYPN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae protein sequence, SEQ ID 786.
                                                                                                                                                                                                                                                     SDQ---ESTTATA----AQPSASSASTAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; Vaccine; bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chevalier F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rusniok C, Chevalier F,
Couve E, Buchrieser C,
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(CNRS ) CNRS CENT NAT RECH SCI.
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Zouine M,
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ADV88332

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                                                                                                                                                                                                                                                178 AIENNKAALATORAQLEAAQLELSAQLTTVQNEKASLIQAKAOAEEAARKAAEAQAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 KAQAEAKAQAESVAKAQAAA------QVESATAPTETVQTQPRTEIKPSNLTAT
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                                                                                                                                                               1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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                                                                                                                                                                                                                                                                                                                                                                 TIAONTNALNTOOAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAAAAAA
                                                                                                                                Gaps
equivalent for the present basic patent FR2824074A1. WO200292818A2 contains 6617 sequence whereas the present patent only contains 2344
                                                                                                                                45;
                                                                                                Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frangeul L, Lalioui L;
Poyart C, Trieu-Cuot P,
                                                                                              58.5%; Score 1234.5; DB 8; Length 59.7%; Pred. No. 6.7e-75; ive 43; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 SVANNSSIQVMESNYAGNMSIGNYRGSFNPSASGSVYYIYPN 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 GV-QGGQIQVQEANYAGNQSIGNYRGWFNP---GSVSYIYPN 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; vaccine; bacterial infection.
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Couve E, Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADV81808 standard; protein; 447 AA
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(CNRS ) CNRS CENT NAT RECH SCI.
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Zouine M,
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The present invention relates to novel Streptococcus agalactiae

nucleotide sequences (1; ADV78860-ADV78998 and ADV83341-ADV85476) and

nucleotide sequences (1; ADV78860-ADV81203 and ADV831205-ADV83340). The

nucleotide sequences encode polypeptides of S. agalactiae involved in the

nucleotide metabolism, cell membranes, intermediate (central)

cequatory functions replication, fatty acid and phospholipid metabolism,

nucleotide metabolism including purines, pyrimidines and/or nucleosides,

regulatory functions, replication, transcription, translation, protein

transport, adaptation to atypical conditions, sensitivity to medicines

and/or analogues, functions related to transposons, biosynthesis of

cofactors, prostheric groups and transporters, cell membrane proteins and

cellular machinery. (1) are useful for the detection and/or amplification

cofactors, prostheric groups and transporters, cell membrane proteins and

cellular machinery. (1) are useful for the detection and/or amplification

cofactors prostheric groups and transporters, cell membrane proteins and

cellular machinery. (1) are useful for the detection and/or amplification

cofactors prostheric groups and transporters, cell membrane proteins

cellular proteins agalactical composition comprising (1) or (II) are

useful for treatment of a bacterial S. agalactiae infection. The complete

genome of Streptococcus agalactiae is given in ADV81204. Note: The

present patent is an equivalent for the basic patent FR2824074A1, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSATTVATTTATATNEPKVTQPSVVTKAVEAPKAVVSSTPRAVSKPVVRSYDSSNTYPMG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCTWGVKSLAPWVGNYWGNGGQWAASAAAGYRVGSTPSAGAVAVW--NDGGYGHVAYVT 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%; Score 1234.5; DB 8; Length 447; 59.7%; Pred. No. 6.7e-75; ive 43; Mismatches 98; Indels 45;
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                                                                                                 Claim 6; SEQ ID NO 2949; 439pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contains only 2344 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 276; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 447 AA;
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Thu Feb 16 10:07:50 2006

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version -
GenCore (c) 1993
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- protein search, using sw model OM protein

February 15, 2006, 18:03:21; Search time 21.0162 Seconds (without alignments) 1977.789 Million cell updates/sec Run on:

US-10-797-821-31 2110 1 MKKRILSAVLVSGVTLSSAT......SIGNYRGWFNPGSVSYIYPN 432 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 1: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	1059	50.2	392	2	G95258	secreted 45 kd pro
7	1059		392	7	B98124	stre
Ю	683.5	32.4	461	~	7000NC	d 45K pr
4	099	31.3	456	7	E86903	ical
S	543.5	25.8	507	~	S05542	hypothetical prote
9	364	17.3	398	7	AC1763	peptidoglycan lyti
7	350.5	16.6	401	7	AI1387	peptidoglycan lyti
œ	321	15.2	473	7	F70031	cell wall-binding
σ,	266.5	12.6	581	7	E75383	conserved hypothet
10	260.5	12.3	436	~	AH1387	wall
11	257	12.2	437	7	AB1763	wall
12	256	12.1	461	7	H84099	cell wall-binding
13	242.5	11.5	528	~	B75310	rved
14	233	11.0	421	7	JV0057	tolA protein - Esc
15	229.5	10.9	394	7	F90725	membrane spanning
16	229.5	10.9	394	~	G85576	
17	229		971	7	B90835	probable tail fibe
18	229	10.9	973	7	C85693	probable membrane
19	227.5		392	7	F96937	ď
	226.5	10.7	255	~	G90061	hypothetical prote
21	226.5	10.7	265	7	B89837	hypothetical prote
	226.5	10.7	267	7	F90028	_
23	226	10.7	492	7	A28616	Ö.
24	225.5	10.7	166	7	C90029	hypothetical prote
	224.5		688	7	A83179	hyp
	222	10.5	1122	7	G64887	probable tail fibe
27	219	10.4	4776	7	9520	cell wall surface
28	218.5	10.4	1528	7	93	rface antig
29	216	10.2	483	7	A26297	M6 protein - Strep

121

8 6 8

INAIINSKSVSDAINRVSAIREVVSANEKMLOQQEQDKAAVEQKQOENQAAINTVAANQE 180

61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY

KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300

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301 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA

361 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRG 419

279 360

181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240

Htrl7 transducer [	FmtB protein [impo	M24 protein precur	cell surface antig	IgA-specific metal	hypothetical prote	M protein precurso	IgA-specific metal	M protein precurso	probable secreted	transcription acti	extracellular matr	uncharacterized pr	IgA-specific metal	regulatory protein	regulatory protein
D84325	D90011	A28549	A43607	A81937	T13606	S30284	S61314	A60115	T34852	S66736	T31110	B97273	C81169	A26639	S01272
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536	2481	539	1566	1773	1589	436	1561	564	1156	1081	2055	351	1815	555	574
10.1	10.1	10.0	10.0	10.0	10.0	6.6	6.6	9.6	9.6	9.6	9.7	9.6	9.6	9.6	9.6
	213	211	10.5	10.5	210	208.5	208	206.5	206.5	206	204	203.5	203.5	203	202.5
213.5	•		N	~		•									

## ALIGNMENTS

88 69	RESULT 1 G95258
Sec	secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
ΰ	C;Species: Streptococcus pneumoniae
ΐυ	C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
2,0	C;Accession: G95258
R	R, Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
o	, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nsc	nson, T.; Hickey, E.K.; Holt, I.E.
SC	Science 293, 498-506, 2001
A;	Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A.	A, Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;	A; Reference number: A95000; MUID:21357209; PMID:11463916
A;	A; Accession: G95258
Α;	A;Status: preliminary
A;I	A; Molecule type: DNA
A;1	A;Residues: 1-392 <kur></kur>
A;	A; Cross-references: UNIPROT: Q97N55; UNIPROT: Q8DMY4; UNIPARC: UPI0000051B81; GB: AE005672;
A;	A;Experimental source: strain TIGR4
ີ່ເວ	C, Genetics:
A;(	A;Gene: SP2216
,	Ouery Match 50.2%; Score 1059; DB 2; Length 392;
-	Similarity

4

Gaps

52;

91; Indels

75; Mismatches

218; Conservative

Matches

g ò

120

9

9

1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG  suk

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A;Accession: E86903
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-456 <STO>
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A,Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000651B81; GB:AE007317; C;Genetics:
A;Gene: gsp-781
                                                                                                                                          C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98124
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHofff, B.S.;
P. R; LeBlanc, D.J.; Lee, L.W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
V. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Reference number: A97872; MuID:21429245; PMID:11544234
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C;Species: Lactococcus lactis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JN0097
R;van Asseldonk, M.; Rutten, G.; Oteman, M.; Siezen, R.J.; de Vos, W.M.; Simons, Gene 95, 155-160, 1990
                                                                                                                               stress protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6)
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TSAAAAGFRTGSTPQVGAIACWNDGGYGHVAVVTAVESTTRIQVSESNYAGNRTIGNHRG 374
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WFNPTTTSEGFVTYIY 390
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                             WFNP----GSVSYIY
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A;Molecule type: DNA
A;Residues: 1-392 <KUR>
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hypothetical protein usp45 [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis Simportin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;File: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Reference number: A66625; MUID:21235186; PMID:11337471
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A,Title: Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis A,Reference number: JN0097; MUID:91071599; PMID:2123812
A;Accession: JN0097
A;Status: preliminary
A;Rotcus: preliminary
A;Rotcus: 174e: VAN>
A;Residues: 174e: VAN>
A;Cross-references: UNIPARC:UPI000016D72B; GB:M35374
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180 SLDSQAQELTSQQAELKVATLNYQATIATAQDKKQALLDBKAAAEKAAQEAAKKQAAYEA
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Best Local Similarity 34.1%; Pred. No. 3.1e-25;
Matches 163; Conservative 111; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                               Query Match 32.4%; Score 683.5; DB 2; Best Local Similarity 35.3%; Pred. No. 2.3e-26; Matches 170; Conservative 107; Mismatches 135;
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Db 301 NSFIGSSTEESTVPESFQESTPANTESSSSSNINVNNNTNNSTNNSTT 360	Oy 333	Qy 357GQWAASAAAAGYRVG-STPSAGAVAVWND-GGYGHVAYVTG 395	Qy 396 VQGGQIQVQEANYAGNQSIGNYRGWFNP 423	RESULT 6 AC1763	peptidoglycan lytic protein P45 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Dete: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AC1763	R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; B.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fs D.; Jones, L.M.; Karst, U.	A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Piitle: Comparative genomics of Listeria species. A.Feference number: ABIO77; MUID:21537279; PMID:11679669	A, Status: preliminary A, Molecule type: DNA A, Rosidues: 1-398 «GLA» A, Residues: 1-398 «GLA» A, Cross-references: UNIPROT: Q927Y8; UNIPARC: UP10000CC935; GB: AL592022; PIDN: CAC97875 A, Experimental source: strain Clip11262 C, Genetics: A, Gene: spl	Query Match 17.3%; Score 164; DB 2; Length 198; Best Local Similarity 27.4%; Pred. No. 5.4e-11; Matches 115; Conservative 88; Mismatches 145; Indels 72; Gaps 16;	QY 1 MKKRILSAV-LVSGYTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQAAQAQVNTIQ 59	60 GQVSALQTQQAELQAENORLEAQSATLGQQ1QTLSSKIVARNESLKQQARSAQKSNAATS :	120 YINAIINKSVSDAINKVSAIREVVSANEKMIQQQEQDKAAVEQKQQENQAAI  :   :::::   :     :      ::  :     :    119 YLEVILDAENLSDLVGRVSAVNQLVDSDKSILEDQQKDEKALKTKQTAVKKKQEEQATAI	173 NIVAANOETIAQNINALNIYQAQDEAAQLALQAELITAQDQKATLVAQKAAEEAARQAA 	233 AAQAAAEAKAAABEKALQEQAAQAQAAANNINIQATUASUQQAAANNIQAAQTADSIDQ 		Qy 346APWYGNYWGNGGGMAASAAAAGYRVGSTPSAGANAWW-DGGYGHYAYYTGVGGGGT 401
: :  :	61 QVSALQTQQABLQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120	121 INAIINSKSVSDAINRVSAIREVVSANEKMLOQQEQDKAAVEQKQQENQAAINTVAANQE 180 :: :     ::	181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240 ::	241 KAAAEAKALQEQAAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAV 298 :	299 NNSDQESTTATAAQPSASSASTAAVAANTSSANTYPAG 336	337 QCTWGVKSLAPWVGNYWGNGGOWAASAAAGYRVGSTPSAGAVAV 381	SADFVGYANSPYGHVAYVTGV-QGGQIQVQEANYAGNQSIGNYRGWFNPGSVSYIYPN 43	RESULT 5 805542 hypothetical protein, 54K - Enterococcus faecium C;Species: Enterococcus faecium C;Dete: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: 805542	, P.; Moesch, H.U.; Solioz, M. Acida Res. 17, 6724, 1989 A protein of unusual composition from Enterococcus faecium. Ance number: S05542; MUID:89385998; PMID:2780297	16421; EMBL:M260 nd 223 as Lvs	07; 101;	10 LVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQ 69   ::	70 AELQAENQRIJEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKS 129 	130 VSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQETIAQNTNAL 189 	190 NTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAABEBAARQAAAAQ 235 	

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12.6%; Score 266.5;
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Matches 111; Conservative
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C;Species: Listeria monocytogenes
C;Sateria C; Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: Al1387
C;Accession: Al1387
C; Schueter, D; Buchaud, E; Durand, L; Dussurget, O; Butian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.S.; Azatt, U.S.; Azatt, U.S.; Almerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species.
A;Reference number: Al1387
A;Status: preliminary
A;Residues: L-401 <GLA>
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c; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #text_change 09-Jul-2004
C; Bacossion: F70031
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A;Experimental source: strain EGD-e
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A. A; Lite: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: F70031
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-473 < KUN>
A; Cross-references: UNIPROT: P40767; UNIPARC: UP10000060AE1; GB:Z99121; GB:AL009126; NID:G; A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generi
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Baccies: Deinococcus radiodurans
C;Bacces: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75383
R;Mitte, O.; Bisen, J.G.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; R.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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A;Itle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75280; MUID:20036896; PMID:10567266
A;Accession: E75383
A;Residues: 1-581 <WHI>
A;Molecule type: DNA
A;Residues: 1-581 <WHI>
A;Residues: 1-581 <WHI>
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1549
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1549
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Ender: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                VSALQTQQAELQAENQRLEAQSATLGQ---QIQTLSSKIVARNESLKQQARSAQKS---N 115
                                                                                                                                                                                                                                                                                                                                                     273 VRERTRLEEERRRRLEEERRRREAEARRIREAQERARKEAERLARIRAEQERKAREAAEA 332
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                                                Indels 149;
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                                                Mismatches 174;
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Mismatches 160;
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                                                                                                                                                                                               Coll wall-binding protein BH3600 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Datollus halodurans
C;Species: Datollus halodurans
C;Accession: H84099
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 256; DB 2; Length 461;
; Pred. No. 1e-05;
88; Mismatches 171; Indels
--SSASTAAVAANTSSANTY--PA-GOCTWGVKSLA-PWVGNYWGN-
                                                                                           --GSTPSAGAVAVWNDGGYGHVAYVTGVQGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| |: | : | GPHLHFEVHEGSYRGSSSAVNPMNYIN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G---QIOVOEANYAGNOSIGNYRGWFN 422
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20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conservative
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Best Local Similarity
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A; Residues: 1-461 <STO>
                                                                          AAAAGYRV-
                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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RESULT 13

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M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Malsi, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Feference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75310
A;Astus: preliminary
A;Rederic radiodurans R1.
A;Rederic R1538 AWIS
A;Residues: 1-528 AWIS
A;Cross-references: UNIPROT:Q9R5J1; UNIPARC:UPI00000C1A76; GB:AE002048; GB:AE000513; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tolds protein - Escherichia coli (strain K-12)
C;Species: Bacherichia coli
C;Species: Bacherichia coli
C;Species: Bacherichia coli
C;Species: Bacherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Bactesion: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J; Bacteriol. 111, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produc A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Resion: JV0057
A;Resion: JV0057
A;Resions: JV0057
A;Resions: JV0057
A;Resions: JV1 1-15 LiEV
A;Resions: JV0057
A;Resions: JV0057
A;Resions: JV0057
A;Experimental source: strain JM105
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A;Fille: The complete genome sequence of Escherichia coli K-12.
A;Reseasion: JM105
A;Fille: The complete genome sequence of Escherichia coli K-12.
A;Reseasion: JM105
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A;Fille: The complete genome sequence of Escherichia coli K-12.
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A;Molecule type: DNA
A;Residues: 1-421 <BLAT>
A;Residues: 1-421 <BLAT>
A;Cross-references: UNIPARC;UPI0000137105; CB:AE000177; GB:U00096; NID:gl786955; PIDN:AAC
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t}
C;Genetics:
P.; McDonald, L.; Utterback, T.; Zalewski, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESL----KQQARSAQKSNAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 TSYINAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 EQE--AQNAQTRANAAQARTEELQRRAAAQATAQAAQTRAAQASQKAQQASARAEQVRE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- DASVROAQOAAQTOLGOVRTG 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 LRAARTER-----EAARSEAOKA--GOEREAAROELAAARONLASAOOEOARLTKOAODL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2330 QAAAAQAAAEAKAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 242.5; DB 2; Length 29.1%; Pred. No. 5.4e-05; ive 56; Mismatches 131; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 AAQQVAQA-----QQQAQAQAHRPSSA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain R1
C, Genetics:
A, Gene: DR2133
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Best Local S:
Matches 95
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C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75310
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
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347
115 NAATSYINAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINT 174
                                    119 QАЕБААКQАБLКОКОАББАААКАААДДАКАКАЕДДОКААББААККААДДАККАЕДДАКА 178
                                                                                                                          179 даедоккаедарадыкккаедаедардаедккадаекдаркка---декдадекдарк 235
                                                                                                                                                                                                              236 KAAAEKAAADKKAAA-AKAAAEKAAAKAAA-----EADDIFGELSSGKNAPKTGGG 286
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                                                                             175 VAANQETIAQNTNALNTQQAQLBAAQLNLQ---ABLTTAQDQKATLVAQKAAAEEAA--R
                                                                                                                                                                   230 QAAAAQAAABAKAAAABAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDS
                                                                                                                                                                                                                                                       290 TDQSAAQAVNNSDQESTTATAAQ-PSASSASTAAVAANTSSANTYPAGQCTWGVKSLAP-
                                                                                                                                                                                                                                                                                                                                                348 -WVGNYWGNGGQWA-ASAAAAGYRVGSTPSAGAVAVW 382
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Job time : 24.0162 secs
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90725
E;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. B, 11-22, 2001
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90725
A;Status: preliminary
A;Residues: 1-394 cHXY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q8X965; UNIPARC:UP1000000086A; GB:BA000007; PIDN:BAB34197.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 AAADNTQAAQTGDSTDQSAAQAVNNSDQESTTATAAQ-PSASSASTAAVAANTSSANTYP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GQVSA-----LQTQQA--ELQ----AENQRL-EAQSATLGQQ1QTLSSKIVARNES 103
                                                                                                                                                                                                                                                                                                                                                                             LKQ-QARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QKQQENQAAI--NTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL-TTAQDQKATLV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AOKKAEAAAALKKKAEAAEAAAEARKKAATEAAEKAKAEAEKKAAAEKAAADKKA--A 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ELSSGRNAPKTGGGAKGNNASPAGSGNTKNNGASGADINNYAGQIKSAIESKFYDASSYA 359
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                                                                                                                                                                                                                                                         ILSAVLVSGVTLSSATTLSAIKADDFDAQIASQ-----DSKINNLTAQQQAAQAQVNTIQ 59
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                   Score 233; DB 2; Length 421;
Pred. No. 0.00012;
                                                                                                                                                                                                                66; Mismatches 178; Indels
                                      A Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
F;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                        11.0%;
28.5%;
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Best Local Similarity 27.5%
Matches 109; Conservative
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Best Local Similarity 28.5'
Matches 117; Conservative
               Map position: 17 min
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MEDLINE=21481971; PubMed=11598068;

DOI=10.1128/IAI.69.11.6931-6941.2001;

Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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0938V2,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
51-Eptococcus mutans.
Bacteria, Firmicutes; Lactobacillales; Streptococcases;
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44648 MW; E769B2504AEE50E9 CRC64;
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Infect. Immun. 69:6931-6941(2001).
EMBL. AVOMGA12, AAK94502.1; -; Genomic_DNA.
InterPro; IPR007921; CHAR.
InterPro; IPR00148; SibA.
Pfam; PF0527; CHAP; 1.
PRINTS; PR0185; SIBARKOTEIN.
PROSITE; PS50911; CHAP; 1.
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0802748 LISINA
091788 LISINA
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                          DOI=10.1128/IAI.69.4.2493-2501.2001;
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by
differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
    TIAONTNALNTOQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAT
                                                                                             KAAAEAKALOEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
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Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
"A 60-kilodalton immunodominant glycoprotein is essential for cell
wall integrity and the maintenance of cell shape in Streptococcus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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Immunodominant glycoprotein IDG-60 (Glucan-binding protein
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J. Dent. Res. 79:224-224 (2000).
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MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
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MEDLINE=21481977; PubMed=11598074;
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Q9AG98;
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STRAIN=3SN1;
MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6541.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
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44652 MW; 3F88ECB9A1F3BE4F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 8.3e-86;
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InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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1; Mismatches
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PROSITE; PS50911; CHAP; 1.
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.",

Infect. immun. 69:693-6941(2001).

EMBL; AYO46410; AAK94500.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.

PRINTS; PR01625; CHAP; 11bA.

PRINTS; PR01625; SIBAPROTEIN.

PROSITE; P805091; CHAP; 1.

SEQUENCE 431 AA; 44620 MW; 464FE3B563FB7E51 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
butative secreted antigen GppB/SagA; putative peptidoglycan hydrolase.
Names-gpbB; OrderedLocusNames-SMU.22;
Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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QBDWM3;
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DOI=10.1128/IA1.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
Duncan M.J.;
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                                                                                                                                                                                                                                 44592 MW; 3EBE21FC5E47232E CRC64;
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Last annotation update)
               Infect. Immun. 69:631-6941(2001).

EMBL, AF938445; AAK08104.1; -; Genomic_DNA.

EMBL; AY046411; AAK08104.1; -; Genomic_DNA.

InterPro; IPRO01921; CHAP.

InterPro; IPRO0146; SibA.

Pfam; PP05257; CHAP; 1.

PRINTS; PR01852; SIBAPROTEIN.

PROSITE; PS50911; CHAP; 1.

SEQUENCE 431 AA; 44592 MW; 3EBR21FFFF77777
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Pred. No. 4e-85;
2; Mismatches
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Q938V3;
01-DEC-2001 (TrEMBLrel. 19, C.
01-DEC-2001 (TrEMBLrel. 19, L.
01-MAR-2004 (TrEMBLrel. 26, L.
Glucan-binding protein B.
                                                                                                                                                                                                                                                                                98.7%;
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Best Local Similarity 99.1
Matches 428; Conservative
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STRAIN=SJ32;
            clinical isolates.";
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NCBI_TaxID=1309;
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MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
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Query Match 98.6%; Score 2079.5; DB 2; Length 431; Best Local Similarity 98.8%; Pred. No. 6.1e-85; Matches 427; Conservative 2; Mismatches 2; Indels 1;
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61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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J. Bacteriol. 183:1175-1183(2001).
EMBB. AJ77292; CAC218144.1; -; Genomic_DNA.
Interpro; IPR007921; CHAP.
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             protein B and analysis of genetic diversity and protein production in
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Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
Chhatwal G.S.;
                                                                                                                                                                                                                                                                                             DB 2; Length
                                                                                                                                                                                                                                                                                          98.4%; Score 2075.5; DB 2; Length 98.6%; Pred. No. 9.2e-85; ive 2; Mismatches 3; Indels
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                                                                                                                                                                Pfam, PF05257, CHAP; 1.
PRINTS, PR01882; SIBAPROTEIN.
PROSITE; PS50911, CHAP; 1.
SEQUENCE 431 AA, 44650 MW; 05D38D8BEC4609F CRC64;
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                                  clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL. AV046414; AAK94504.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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Q9AKA4;
01-JUN-2001 (TEMBLFEl. 17,
01-JUN-2004 (TEMBLFEl. 17,
01-MAR-2004 (TEMBLFEl. 26,
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                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                  Score 2079.5; DB 2; Length 431; Pred. No. 6.1e-85; 2; Mismatches 2; Indels 1;
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Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                     44620 MW; 2D1CA685248CCD3E CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
EMBL; AE014855; AANS7811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam, Pf05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS0911; CHAP; 1.
Complete proteome.
SEQUENCE 431 AA; 44620 MW; 2D1CA685248CCD3E CRC6
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MEDLINE=21481971; PubMed=11598068;
                                                                                                                                                                                                                                                                     98.6%;
98.8%;
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Matches 427; Conservative
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PRINTS; PR01852; SIBAPROTEIN.
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                                                                                     TIGR; SAG0017; -.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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QBE7X9_STRA3 PRELIMINARY;
Q8E7X9;
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Matches 276, Conservative
                                                                                                                                                                                Pfam; PF05257; CHAP; 1.
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SEQUENCE 447 AA
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MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Wassella M., Masignani V., Cieslewicz M.J., Elsen J.A., Petcrson S.N., Wassella M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewiß M.R., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobnin E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Ranado D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                     DB 2; Length 447;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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46681 MW; F4DB14B0A5F962C8 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                     58.5%; Score 1234.5; DB 59.7%; Pred. No. 2.1e-47
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                            Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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QBE2H1;
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447 AA;
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BUDLINE=22242568; PubMed=1234221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
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emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
EMBL; AEO14192; AAM98925.1; -; Genomic_DNA.
TIGR; SAG0017; -.
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Name-posB; OrderedLocusNames-gbs0016;
Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Mol. Microbiol. 45:1499-1513(2002).
EMBL, AL766843; CAD45661.1; -; Genomic_DNA.
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PubMed=15272401; DOI=10.1086/422697;
PubMed=15272401; DOI=10.1086/422697;
PubMed=15272401;
Doi=10.1086/422697;
PubMed=15272401;
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E., Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus metagenome: complete genome sequence of a macrolide-resistant serotype M6 strain.",
J. Infect. Dis. 190:727-738(2004).
EMBL: CD000003; AAT86152.1; -; Genomic_DNA.
                                                                                                                                                         1 MKKRILSAVLVSGVTLGTAAV--TVNADDFDSKIAATDSVINTLSGQQAAAQNQVTAIKG
                                                                                                                                                                                                   1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                             181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAAAAAA
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                                                                                                                        Gaps
                                                                                                                        45;
                                                                                                  DB 2; Length 447;
                                                                                                                       98; Indels
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                              447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                 58.5%; Score 1234.5; DB 59.7%; Pred. No. 2.1e-47;
                                                                                                                                                                                                                                                                                                                                                                  SDQ---ESTTATA-----AQPSASSASTAA-----
                                                                                                                       43; Mismatches
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InterPro; JER0016; -.
InterPro; JER007221; CHAP.
InterPro; JER00148; SibA.
Pram; PF0527; CHAP; 1.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 447 AA: Accor.
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QSXELL;
                                                                                                                       Matches 276; Conservative
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NUCLEOTIDE SEQUENCE.
                                                                                                              Best Local Similarity
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QSXEL1 STR
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C STRAIN=MASS122 / Serotype M18;

MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

A Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

A Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

A Kapur V., Daly J.A., Vassy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype M18 rapur A streptococcus strains associated with acute rheumatic fever I proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

R EMBL, AEO9955; AAL96849.1; -; Genomic_DNA.

R InterPro; IPR009148; SibA.

R PRINTS; PR01825; SIBAPROTEIN.

R PRINTS; PR01825; SIBAPROTEIN.
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umatic fever
                                                                                                                                         Length 398;
                                                                                                                                   51.8%; Score 1093; DB 2; Length 3 53.8%; Pred. No. 3.5e-41; ive 58; Mismatches 106; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                 SDCEDA78CB863B60 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                 398 AA; 42028 MW;
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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Q7CNQ7;
                                                                                                                                                                   Best Local Similarity 53.8
Matches 233, Conservative
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NCBI_TaxID=301451;
                                                    Complete proteome. SEQUENCE 398 AA;
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phage-encoded toxins, the high-virulence phenotype, and clone
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PROSITE; PS50911; CHAP; 1.
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SEQUENCE 398 AA;
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MEDLINES22663278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 Errain Of Streptococcus pyogenes reveals a
"Genome sequence of an M3 Errain Of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                                                           1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                            1 MKKRILSAVLVSGVTLGAATT---VGAEDLSTKIAKQDSIISNLTTEQKAAQNQVSALQA
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MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
                                       Length 398;
                                       51.8%; Score 1093; DB 2; Length 3 53.8%; Pred. No. 3.5e-41; ive 58; Mismatches 106; Indels
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Streptococcus pyogenes (serotype_M3).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
               42028 MW; 5DCEDA78CB863B60 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Genome Res. 13:1042-1055(2003)
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OrderedLocusNames=SP80015,
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Q8P318; Q7CFL7;
                                                                  Matches 233; Conservative
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NUCLEOTIDE SEQUENCE
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                398 AA;
                                                     Best Local Similarity
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NCBI_TaxID=301448;
 Complete proteome
SEQUENCE 398 AA
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61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnalle B., Prozzi D.,
Ngui K., Mauy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
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OSMGK4;

O1-FBB-2005 (TrEMBLrel. 29, Created)
O1-FBB-2005 (TrEMBLrel. 29, Last sequence update)
O1-FBB-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (PosB).

Name=pcsB, OddredClocusNames=stu0022;
Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                               398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002)
EMBL; BA000034; BAC61110.1; -; Genomic_DNA.
EMBL; AB014136; AAM78621.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.8%; Score 1093; DB 2; I
Best Local Similarity 53.8%; Pred. No. 3.5e-41;
Matches 233; Conservative 58; Mismatches 106;
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240

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Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELETTEAGLTTQQAELEAAQVTLAAELATAQNEKTSLVSAKSTAESVAASTAASVAQSQA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSTDQSAAQAVNN-----SDQESTTATAAQPS----ASSASTAAV-----AANT- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVOPESAAPAVSEAPASVAPVATSEAPATSEAPASVAPVATSEAAPAVSEAPAPAAETH 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 KVSAASTPNTYPVGQCTWGVKSLAPWAGNNWGNAKNWIASAQAAGHSVGTTPVAGAIAVW 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 AAEAKA-----AAEAKALQEQAAQAQAAANININTQATDASDQQAAAADINTQAAQTG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ND-GGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRGWFNP-----GSVSYIYP 431
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                                                                                                                                                            Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P., Decaris B., Leblond Bourget N.;
"cse, a Chimmeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Sergegation in Streptococcus thermophilus.";
J. Bacteriol. 187:2737-2746(2005).
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PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1092.5; DB 2; Length; Pred. No. 4.4e-41; 73; Mismatches 107; Indels
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Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 187;2737-2746 (2005).

EMBL; CD000023; AAV59752.1; -; Genomic_DNA.
EMBL; AY70643; AAW82752.1; -; Genomic_DNA.
INTERPRO; IPR007921; CHAP.
INTERPRO; IPR009148; SibA.
PEMM; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS0911; CHAP; 1.
COMDICTE PROCEOME.
SEQUENCE 474 AA; 48142 MW; IBAC6A9E0A0A200
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Biotechnol. 22:1554-1558(2004)
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51.7%;
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QSM212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 AAEAKA-----AAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTG
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                                                                                                  "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
BMBL: CP000024; AAV616411; -; Genomic_DNA.
InterPro; IPR00921; CHAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D., Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D., Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J., Goffeau A., Hols P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                51.8%; Score 1092; DB 2; Length 485; 50.9%; Pred. No. 4.8e-41; ive 71; Mismatches 107; Indels 6
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STRAIN=SF370 / ATCC 700294 / Serotype
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                                                                                                                                                                                                                                                                                  Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;

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Search completed: February 15, 2006, 18:09:15 Job time : 127.762 secs
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386 WFNPTGVTFIYPH 398
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QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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             Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar P.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.; Chifton S.W., Roe B.A., McLaughlin R.E.; Processes B.A., McLaughlin R.E.; Processes Processes B.A., McLaughlin R.E.; Processes B.A., McLaughlin R.E.; Processes B.A., Brain Of Streptococcus pyogenes.", Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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NUCLEOTIDE SEQUENCE.
Fagan P.K., Reinscheid D., Gottschalk B., Chhatwal G.S.,
"Identification and characterization of a novel secreted protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQ-GGQIQVQEANYAGNQSIGNYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          51.5%; Score 1087; DB 2; Length 398;
53.6%; Pred. No. 6.6e-41;
tive 58; Mismatches 107; Indels 36;
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR004474; AR433158.1; -; Genomic_DNA.
EMBL; AR131999; AAL73135.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR00148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
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ORGANISM: Streptococcus pneumoniae
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US-09-107-433-3230
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109, App
5441, Ap
5453, Ap
6321, Ap
1682, Ap
2870, Ap
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2110
1 MKKRILSAVLVSGVTLSSAT......SIGNYRGWFNPGSVSXIXPN
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5.1.7
Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
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US-09-107-532A-670

US-09-134-000C-5990

US-09-071-035-482

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seq length: 200000000
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Match
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                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                           OM protein
                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
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FOR DIAGNOS
                                                                                                                                                                                                                                                                  Sequence 7646, Ap
Sequence 7647, Ap
Sequence 33, Appl
Sequence 4, Appli
                                                                13861, A
1, Appli
3, Appli
1, Appli
1, Appli
12755, A
6, Appli
6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3230, Application US/09107433

Patent No. 6800744

GENERAL INPORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                        Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Mascachusetts
COUNTRY: USA
                                                                                   US-08-006-6768-1
US-08-282-845-2
US-08-4284-144-1
US-08-4270-77-44973
US-09-489-039A-12755
US-08-795-475-6
US-09-949-016-7646
US-09-949-016-7646
US-09-949-016-7647
US-08-949-016-7647
US-08-949-016-7647
US-08-470-950-4
US-08-687-956A-23
US-09-489-039A-12307
US-09-902-540-14908
US-09-902-540-13861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USAN

THE OLD STATE

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM 1809660

COMPUTER: CUNKNOWN>
OPERATING SYSTEM: CUNKNOWN>
SOFTWARE: CUNKNOWN>
CURRENT APPLICATION DATA:

APPLICATION NUMBER: G0/09/107,433
FILING DATE: 30-Unn-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/05131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051533
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERRNCE/DOCKET NUMBER: 40,489
REFERRNCE/DOCKET NUMBER: 40,489
REFERRNCE/OFKET NUMBER: 40,489
RELEPRAM: (781)893-807
TELEFRAM: (781)893-8277

INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERIFICS:
LENGTH: 399 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                    US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THERAPEUTICS
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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                                       INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                   181 TIAONTNALNTOOAOLEAAOLNLOAELTTAODOKATLVAOKAAAEEAAROAAAAOAAAEA 240
                                                                                                                                                                                                 241 KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
                                                                                                                                                                                                                                                                                                       361 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRG 419
                                                                                                                                                                                                                                                                              301 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 461;
                                                                                                                                                                                                                          241 KRASQQQSV-----LASANTNLTAQVQAVSESAAAPVRAKVRPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%; Score 681.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suri, Bruno
APPLICANT: Schmitz, Albert
TITLE OF INVENTION: Bacterial Vectors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,205
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: GB 9006400.7
FILING DATE: 22-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTAINS
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOWNTER: IBM PC COMpatible
TOWNTER: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-186-222-2
; Sequence 2, Application US/08186222
; Patent No. 5559007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Villamizar, Joann
REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||
375 WFNPTTTSEGFVTYIY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                         WFNP----GSVSYIY 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (914)785-7121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (914)347-5769
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino ació
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-186-222-2
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US-09-583-110-4374
Sequence 4174, Application US/09583110
Sequence 4174, Application US/09583110
Senert No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
CURRENT FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                       181 TIAONTNALNTOOAQLEAAQLNLOAELTTAQDOKATLVAQKAAAEEAARQAAAAAQAAEA 240
                                                                                                                                                                                                                                                                                                                                                                                 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 TSAAAAGFRTGSTPQVGAIACMNDGGYGHVAVVTAVESTTRIQVSESNYAGNRTIGNHRG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVSALÇTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                                                    QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                            361 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRG
                                                                                                                       1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNYWGNAA
                                                                                Gaps
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                                                                                52;
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                                       Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                Indels
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Best Local Similarity 50.0%; Pred. No. 4.2e-73;
Matches 218; Conservative 74; Mismatches 92;
                                         DB 2;
                                                           3.6e-73
                                       50.2%; Score 1059; DI
50.0%; Pred. No. 3.6e-
tive 75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLAGEMY FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PRIOR DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR PILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFNP-----GSVSYIY 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFNPTTTSEGFVTYIY 397
                                                                                Matches 218; Conservative
                                           Query Match
Best Local Similarity
    JS-09-107-433-3230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-583-110-4374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 NIQAAQIGDSIDQSAAQAVNNSDQESIIA-----IAAQPSASSASIAAVAANISS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| | | : | | | : | | 359 ESTTPAPITIPSTDQSVDTGNGT-GSSTPAPIPTPEQPKPVTPAPAPSGSVNGAAIVAE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OVSALQTQQAELQAENQRLEAQSATLGQQ1QTLSSK1VARNESLKQQARSAQKSNAATSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AAEE
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APPLICANT: Fritz, Chrisian
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REPERENCE: 07334/060001
CURRENT APPLICATION NUMBER: US/09/222, 938A
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAVW-NDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWFNP 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TIAONTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.7%; Score 584.5; DB 2; Best Local Similarity 30.4%; Pred. No. 1.1e-36; Matches 160; Conservative 92; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...525
SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67, Application US/09222938A Patent No. 6437108 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION
                         TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5095:
                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- MAGN -- - YWGNG ---
                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-107-532A-5095
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                                                                                           120 MDAVVNSKSLTDVIQKVTAIATVSSANKQMLEQQEKEQKELSQKSETVKKNYNQFVSLSQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAAAEAKALQEQAAQAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQ----SAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAVNNSDQESTTATAAQPSASSASTAAVAANTSS-------ANTY 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 PAGQCT---WG-----VKSLAPWVGNYGOGGWAASAAAAG--YRVGSTPSAGAVA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 AVGGCTDYVWQYPAAQGIYIRNIMP-----GNGGQWASNGPAQGVLHVVGAAP--GVIA 402
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                                                                                       1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAVNTIQG
                                                                                                                           1 MKKKIISAILMSTVILSAAAPLSGVYADT-NSDIAKQDATISSAQSAKAQAQAQVDSLQS
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                                Gaps
                             69
                             Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                             Matches 170; Conservative 106; Mismatches 136;
Pred. No. 3.4e-44;
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATINGALO, Bamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: <Unknown>
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35.3%;
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Best Local Similarity
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US-09-107-532A-5095
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GENERAL INFORMATION:
APPLICANT: Gil H. Choi
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                ----NPGGSG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                  307 ESTITIQETITISSTETESVVITPVAAAPEKEKEVPVTNPTTPEKGNEAKPGNGGVTSGKQA 366
                                                                                                                                                      375 SAGAVAVWNDG-----GYGHVAYVTGVQGQIQVQBANYAGNQSIGNYRGWFNPGSVS 427
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                                                                                                                                                                             427 QPGDVVQYESAXSPDSWIGGVHTVLVTGVSGGSVQIVEAN----
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: PERCETA 466/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CAPRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.7%; Score 500.5; DB 2; 30.7%; Pred. No. 2.4e-30; iive 88; Mismatches 175;
    DOSAAQAVNNSDQES----TTATAAQP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: A. Anders Brockes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 482:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Matches 139; Conserva
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STATE: Maryland
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US-09-071-035-482
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: LYAIN DOUCETLE-Stamm et al
APPLICANT: LYAIN DOUCETLE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BATEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                                                                                                                                                                                                                                                                      61 QVSAIQAEQSNLQAENDRLQAESKKLEGEITELSKNIVSRNQSLEKQARSAQTNGAVTSY 120
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                                                                                                                                  Query Match 26.6%; Score 561; DB 2; Length 210; Best Local Similarity 55.2%; Pred. No. 2e-35; Matches 116; Conservative 45; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TIAONTNALNTOQAQLEAAQLNLQAELTTA 210
    FastSEQ for Windows Version 3.0
                                                                            ; ORGANISM: Streptococcus pneumoniae US-09-222-938A-67
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US-09-134-000C-5990
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SOFTWARE: PatentIn version 3.1
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SOFTWARE: Fas
SEQ ID NO 67
LENGTH: 210
TYPE: PRT
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Sequence 5714, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT FILIANG DATE: 1999-08-13
PRIOR PILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
12;
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                                                                                                              61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
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 51; Gaps
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88; Mismatches 175;
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139; Conservative
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TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
AARQAAAAQAAAEAKAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAA-----AADNT 281
                                                                                                                                                     241 KAKQAAAKPAKAEVK--AEAPVASSSTTEAQAPASSSS--ATESSTQQTTETTPSTDNS 296
                                                                                                                                                                                                           QAAQTGDSTDQSAAQAV-----NNSDQESTTATAAQPSASSASTAAVAANTSSANTYPA 335
                                                                                                                                                                                                                                            ATENTGSSSSEQPVOPTTPSDNGNNGGOTGGGTVTPTPEPTPAPSADPTINALNVLRQSL 356
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Pred. No. 2.4e-30;
                                                         TIAONTNALNTOOAOLEAAOLNLOAELTTAODOKATLVAOKAAAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                             396 VOGGOIQV --- OEANYAGNOSIGNYRGW - FNPG 424
                                                                                                                                                                                                                                                                                                                                                                                  400 APGNSVIMAWYNETNMVTASGSG-HRDWEINPG 431
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COMPUTER: Dell latitude
COMPUTER: Dell latitude
COMPUTER: Dell latitude
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
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SEQUENCE DESCRIPTION: SEQ ID NO: 482:
US-10-206-576-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-206-576-482
; Sequence 482, Application US/10206576
; Patent No. 6913907
; GENERAL INFORMATION:
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30.7%;
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COMPUTER READABLE FORM:
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Best Local Similarity
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APPLICANT: Choi et al.

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410, Key West Avenue
                                                                                                                                                  QESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWAAS 362
                                                                                                                                                                                                                                                                                                                                                                                                          346 ARAAQVEAGGIPNDH----WSRG--DEVIAIMWAPGNSVIMAWYNETNWYTASGSG-HRD 398
61 QEITNLNQRIEKRNEAIKNQARDVQVNGQSTTMLDAVLDADSVADAISRVQAVSTIVSAN 120
                                                                             121 NDLMOOOKEDKOAVVDKKAENEKKVKOLEATEAELETKRODLLSKOSELNVMKASLALEO 180
                                                                                                                        TTAQDQKATLVAQKAAAE-----EAARQAAAAQAAAEAKAAAEAKALQEQA 253
                                                                                                                                                                                                          254 AQAQAAANINNTQATDASDQQAA----AADNTQAAQTGDSTDQSAAQAV-----NNSD 302
                                                                                                                                                                                                                                                                                                                                 QTGGGTVTPTPEPTPAPSADPTINALNVLRQSLG-----LRPVV---WDAGLAASAT 345
                                                                                                                                                                                                                                                                                                                                                                            363 AAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQV---QEANYAGNQSIGNYRG 419
                                        148 EKMLOOQEODKAAVEOKOOENQAAINTVAANOETIAQNTNALNTQQAQLEAAQLNLQAEL 207
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APPLICATION NUMBER: US 09/071,035
FILING DATE: 1988-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369PID1
INFORMATION FOR SEQ ID NO: 484:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
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; SEQUENCE DESCRIPTION: SEQ ID NO: 484:
US-10-206-576-484
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OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 484, Application US/10206576 Patent No. 6913907 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 WEINPG 404
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Patent No. 6448043
Patent No. 6448043
Patent No. 6448043
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                    336 GQCTWGVKSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTG 395
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  : | ::|::| : | ELETYRODLISKQSELNVWKASLALEQSSAESSKAGIEKQKAAAEAEQARLAAEQKAAAE 241
                                                              AAROAAAAQAAAEAKAAAEAKALQEQAAQAAAANNNNTQATDASDQQAA----AADNT 281
                                                                                                                                                282 QAAQTGDSTDQSAAQAV-----NNSDQESTTATAAQPSASSASTAAVAANTSSANTYPA 335
                                                                                                                                                                                                                                                                      G-----LRPVV----WDAGLAASATARAAQVEAGGIPNDH-----WSRG--DEVIAIMW 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQAELQAENQRLEAQSATLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.4%; Score 452.5; DB 2; Length 422; 30.0%; Pred. No. 1e-26; tive 81; Mismatches 166; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                       401 APGNSVIMAWYNETNMVTASGSG-HRDWEINPG 432
                                                                                                                                                                                                                                                                                                               396 VOGGOIOV---QEANYAGNOSIGNYRGW-FNPG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 484:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 30.0%
Matches 128; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-071-035-484
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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                           | : : : | | | | : | | | 367 AAAAGSGNTKNSASGADINNYAGQIKSAIESKFYDASSYAGKTCTLRIK-LAPDGLLLNI 425
                                                                                                255 QAQAAANNINTQATDASDQQAAAADNTQAAQTGDSTD------QSAAQAVNNSDQES 305
                                                                                                                                              310 AAEKAAAD---KAAKAAAAKAAAAKKAAAAKEADGVÖNLLGDLSSGKNAPKTGGGAKGNN 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 ANNINITQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNNSDQESTTATAAQPSASSAS 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3.244, Application US/09710279

Sequence 3.244, Application US/09710279

Batent No. 6703492

GENERAL INFORMATION:
APPLICANT KINMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P013480US
CURRENT FILING DATE: 2000-11-09

CURRENT FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3.244

LENGTH: 257
                                                                                                                                                                                           306 TTATAAQPSASSASTA-----AVAANTSSANTYPAGQCTWGVKSLAP--WVGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SNYNNYQ-----SNNTQSQRTTQPTGGLGASYSTSSSNVHVTTTSA-PSSNGVS
  AA---QINLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEAKAAAEAKALQEQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 VAVWNDGGYGHVAYVTGV-QGGQIQVQEANYAGNQSIGNYRGWFNPGSVSYIY 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 11.2%; Score 237; DB 2; 1 Similarity 34.7%; Pred. No. 1.7e-10; 60; Conservative 27; Mismatches 70
                                                                                                                                                                                                                                                                                              353 WGNGGQWA-ASAAAGYRVGSTPSAGAVAVW 382
                                                                                                                                                                                                                                                                                                                                          426 QSEGGDPALCQAALAAARQAKFPKPPSQAVY 456
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Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-001C-5035
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Fatent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Eneton et. al
APPLICANT: Gary Eneton et. al
APPLICANT: Gary Eneton et. al
APPLICANT: Gary Eneton et. al
APPLICANT: APPLICANT: ON UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
                                                                                                                                                                                              QQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSAN 147
                                                                                                                                                                                                                          148 EKMLOOOEQDKAAVEQKOOENQAAINTVAANQETIAONTNALNTOOAQLEAAQLNLOAEL 207
                                                                                                                                                                                                                                                                                                                          TTAQDQKATLVAQKAAAE------EAARQAAAAQAAAEAKAAAEAKALQEQA 253
                                                                                                                                                                                                                                                                                                                                                                                                                           254 AQAQAAANNNYTQATDASDQQAA----AADNTQAAQTGDSTDQSAAQAV----NNSD 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQV---QEANYAGNQSIGNYRG 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVA-ANQETIAQNTNALNTQQAQLE 197
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                                                                                                                              28 DDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQAELQAENQRLEAQSATLG
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                                                  Gaps
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       Length 422;
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; Score 452.5; DB 2; Length
; Pred. No. 1e-26;
81; Mismatches 166; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella pneumoniae
     21.4%;
  Query Match
Best Local Similarity 30.0°
Matches 128; Conservative
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Best Local Similarity
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Sequence 4539, Application US/09134001C

Sequence 4539, Application US/09134001C

Sequence 4539, Application US/09134001C

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION WOMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
FRIOR PELLOR DATE: 1997-11-08
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4539

LENGTH: 267
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Matches 60; Conservative 26; Mismatches 70; Indels 16; Gaps
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                                                                 OTHER INFORMATION: Description of Artificial Sequence: synthetic; COTHER INFORMATION: amino acid sequence US-09-710-279-3244
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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3295, Ap
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362, Ap
5110, Ap
56483, A
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Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REPERENCE: 25669-018

CURRENT FILING DATE: 2003-03-07

PRIOR PILICATION NUMBER: 60/402,483

PRIOR PILICATION NUMBER: 60/402,483

PRIOR PILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-03-07

PRIOR PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

SEQ ID NO 31

LENGTH 432
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US-10-724-972A-6519
US-10-724-972A-5110
US-10-724-972A-5110
US-09-921-120
US-09-931-496-120
US-09-921-496-120
US-09-921-43A-111
US-09-921-22A-59321
US-09-971-536-69
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100.0%; Pred. No. 3.1e-119;
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; ORGANISM: Streptococcus mutans
US-10-383-930-31
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Sequence 32, Application US/10797821

Publication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
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Sequence 32, Application US/10383930

Sequence 32, Application US/10383930

Publication No. US200040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Tambman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binn;

FILE REFERENCE: 25669-018

CURRENT FILING DATE: 2003-007

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/383,209

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

LENGTH: 432
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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens;
FILE REFERENCE: 25669-020
CURRENT PILING DATE: 2004-03-09
PRIOR PLING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 10/383,930
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR FILING DATE: 2002-03-07
PRIOR PLING DATE: 1999-04-12
PRIOR PLING DATE: 1999-04-12
PRIOR PLING DATE: 1999-04-13
PRIOR PLING DATE: 1999-04-13
PRIOR PLING DATE: 1999-04-13
PRIOR PRILING DATE: 1999-04-13
PRIOR PLING DATE: 1999-04-13
PRIOR PLING DATE: 1999-04-13
PRIOR PLING DATE: 1999-01-08
SPIOR PLING DATE: 1999-01-08
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SPIOR PLING DATE: 1999-01-08
SEQ ID NOS: 45
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                                                                                                                                                                                                                                                 Sequence 31, Application US/10797821; Publication No. US20050031633A1; GENERAL INFORMATION:
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Pred. No. 1.4e-118;
                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 10/389,930
PRIOR PILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR PLING DATE: 2002-03-07
PRIOR PLING DATE: 2002-08-08
PRIOR PLING DATE: 1202-04-12
PRIOR PLING DATE: 1999-04-12
PRIOR PLING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/015,50
PRIOR PLING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/011,50
PRIOR PLING DATE: 1999-04-13
PRIOR PLING DATE: 1999-04-13
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US-10-797-821-32
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Sequence 30, Application US/10797821

Publication No. US20050031633A1

GENERAL INFORMATION

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT APPLICATION NUMBER: 10/383,930

PRIOR PILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 1999-04-12

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/04-13

PRIOR FILING DATE: 1999-04-13

SOFTWARE: PATENTIN UNMER: 60/115,142

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45
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PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
LENGTH: 431
                                                                                                                                                                          TYPE: PRT; ORGANISM: Streptococcus mutans US-10-383-930-30
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Sequence 29, Application US/10797821
; Sequence 29, Application US/10797821
; Publication No. US20050031633A1
; GENERAL INFORMATION:
    APPLICANT: Taubman, Martin A.
    TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
    FILE REFERENCE: 25669-020
; CURRENT FILING DATE: 2004-03-09
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 10/383,930
PRIOR PLILNG DATE: 2002-03-07
; PRIOR PELING DATE: 1999-04-12
; PRIOR PELING DATE: 1999-04-12
; PRIOR PELING DATE: 1999-04-13
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; PRIOR PELING DATE: 1999-04-13
; PRIOR PELING DATE: 1999-01-08
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98.8%; Pred. No. 2.1e-117;
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; ORGANISM: Streptococcus mutans
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; Sequence 29, Application US/10383930
; Sequence 29, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
    APPLICANT: Smith, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OP INVENTION: Immunogenicity of Glucan Binding Protein
    FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR PILING DATE: 2002-08-08
; PRIOR PILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In version 3.2
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                                                                                                    Length 431;
                                                                                                                                                           1; Indels
                                                                                                      Score 2083.5; DB 5 Pred. No. 1.2e-117;
                                                                                                                                                           2; Mismatches
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-30
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; ORGANISM: Streptococcus mutans
US-10-383-930-29
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Squence 33, Application US/10797821
Squence 33, Application US/10797821
Squence 33, Application Wo. US2050031633A1
GENERAL INPORMATION:
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020
CURRENT FILING DATE: 2004-03-09
FRIOR APPLICATION NUMBER: 10/383,930
FRIOR PILING DATE: 2002-03-07
FRIOR PELING DATE: 2002-03-07
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR PILING DATE: 2002-04-12
FRIOR APPLICATION NUMBER: 60/402,483
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: 1999-04-13
FRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
LEMCHH: 431
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US-10-797-821-33
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Best Local S:
Matches 426
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241 KAAAEAKALQEQAAQAQVAA-NNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNN
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VE-10-383-930-33

Sequence 33, Application US/10383930

Publication No. USS0040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT PILING DATE: 2003-03-07

PRIOR PILING DATE: 2003-03-07

PRIOR PILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-09-08

PRIOR PILING DATE: 2002-09-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE PARENT PURS DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 33

LENGTH: 431
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Pred. No. 3.7e-117;
2; Mismatches 3;
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; ORGANISM: Streptococcus mutans
US-10-383-930-33
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Best Local Similarity 98.6%;
Matches 426; Conservative
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RESULT 13
US-10-617-320-3230
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                                                                                      LENGTH: 392
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Publication No. US20050020813A1
Publication No. US20050020813A1
APPLICANT: CHIRON SpA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKRILSAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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                                                                                                                                                              APPLICANT: Zagursky, Robert
APPLICANT: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
TITLE OF INVENTION: SURRACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                51.5%; Score 1087; DB 5; Length 39 53.6%; Pred. No. 1.2e-57; ative 58; Mismatches 107; Indels
                                                                                                      Sequence 600, Application US/10474792
Publication No. US20040236072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-600
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                            420 FNPGSVSYIYPN 431
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US-10-472-928-4652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 TSAAAAGFRTGSTPQVGAIACWNDGGYGHVAVVTAVESTTRIQVSESNYAGNRTIGNHRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TIAONTNALNTQOAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEBAARQAAAAAAAABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OVSALQTQQAELQAENORLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: secreted 45 kd protein (usp45)
OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15904062 (0.E+01)
                                                                                                                                                                                                                                                                                                                                                                                                                               50.2%; Score 1059; DB 5; Length 392; 50.0%; Pred. No. 5.7e-56; Live 75; Mismatches 91; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KRASOOOSV----LASANTNLTAOVOAVSESAAAPVRAKVRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <UNKNOWI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3230, Application US/10617320 Publication No. US20050136404A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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Matches 218; Conservative
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61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: 04944

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-66

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-10-26

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2001-02-09

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PRIOR PELING DATE: 2001-02-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 588.5; DB 4;
30.6%; Pred. No. 1.7e-27;
tive 91; Mismatches 163;
Sequence 57658, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                         Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                               Zyskinď, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: BLITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 30.6
Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TIAONTNALNTOQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 KRASQQQSV-----LASANTNLTAQVQAVSESAAAPVRAKVRPT------ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.2%; Score 1059; DB 5; 50.0%; Pred. No. 5.9e-56;
                                                                                                                                                      APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/05153
ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECHONE: (781,893-5007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Mismatches
                                                                            APPLICATION NUMBER: US/10/617,320 FILING DATE: 10-Jul-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/XEY: misc feature
LOCATION: (B) LOCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
          OPERATING SYSTEM: <Unknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 399 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WFNP----GSVSYIY 430
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Matches 218; Conservative
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RESULT 14 US-10-282-122A-57658

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US-10-154-251-67
is Sequence 67, Application US/10154251
; Publication No. US20030092024A1
; GENERAL INFORMATION:
i APPLICANT: Youngman, Philip
i APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
i TITLE OF INVENTY BY ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 66286-660002
CURRENT APPLICATION NUMBER: US/10/154,251
CURRENT APPLICATION NUMBER: US 10/154,251
FRIOR FILING DATE: 2002-09-16
FRIOR FILING DATE: 2002-05-16
SEQ ID NOS: 102
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 67
LENGTH: 210
FILENCE: PASESEQ for Windows Version 3.0
FILENCE: PASESEQ FOR WINDOWS: US 10/154,251
FRIOR FILENCE: PASESEQ FOR WINDOWS 102
FILENCE: PASESEQ FOR WINDOWS 102
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Sequence 210, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF EQ ID NOS: 763
SOFTWARE: Patentin Version 3.3
SED ID NO 2.00
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1016, AD

1076, AD

256, ADD

56, ADD1

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60, ADD1

3188, AD

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98.8%; Pred. No. 2.3e-112;
iive 2; Mismatches 2;
                                               US-11.019-711-8
US-10-995-561-1016
US-10-995-561-1015
US-10-821-234-1076
US-10-793-626-2964
US-11.069-834-56
US-11-069-834-56
US-11-069-834-60
US-11-069-834-60
US-11-069-834-83
US-11-069-834-83
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US-11-052-554A-83
US-11-052-554A-83
US-11-052-554A-83
US-11-052-554A-83
US-11-052-554A-83
US-11-052-554A-83
US-11-052-554A-83
US-11-052-554A-83
                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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US-11-052-554A-210
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                                                                                                                      February 15, 2006, 18:30:27; Search time 8.33977 Seconds (without alignments) 736.166 Million cell updates/sec
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2110
1 MKKRILSAVLVSGVTLSSAT......SIGNYRGWFNPGSVSYIYPN
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Maximum Match 100%
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Maximum DB
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No.
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; Sequence 358, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   95; Conservative
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Matches 95; Conserv
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   US-11-052-554A-352
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Matches 143;
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2006-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR PLING DATE: 2004-07-20
PRIOR PLING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
                                                   420
SDQESTTATEAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA 359
                                                                     ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAQAAAEA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
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Best Local Similarity 53.8%; Pred. No. 5e-56;
Matches 233; Conservative 58; Mismatches 106; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-252
                                                                                                                                                                                                                                          ; Sequence 252, Application US/11052554A; Publication No. US20050288866A1; GENERAL INFORMATION:
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WFNPTGVTFIYPH 398
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LENGTH: 398
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Sequence 352, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
SROOF FILING DATE: 2004-07-30
FRIOR FILING DATE: 2004-07-30
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT PAPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: UN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-30
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
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25.3%; Pred. No. 6.7e-17;
tive 78; Mismatches 186; Indels 158; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%; Score 436.5; DB 7;
44.2%; Pred. No. 7.9e-19;
iive 25; Mismatches 60;
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380 AVWNDGGYGHVAYVTGV-QGGQIQVQEANYAGNQSIGNYRGWFNPGSVSYIY
                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.9%; Score 229.5; DB 7; Best Local Similarity 27.5%; Pred. No. 1.1e-06; Matches 109; Conservative 62; Mismatches 177;
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US-11-052-554A-3
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                                                                                                                             122 GKRKLSLS----APQLSLKQGGLQLFSKLKPSAADQLFSAVWSDENQQDDLHWYTADADG 177
                                                                                                                                                                             -----IREVVSANEKMLQQQEQD----KAAVE-QKQQENQAAINTVAAN 178
                                                                                                                                                                                                    -----OETIAONTNALNIQQAQLEAAQLNLQAE-- 206
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                                                                                                                                                                                                                                                                                                                                       207 ------LTTAQDQKATLVAQKAAAEEAARQAAAAAAAAAAA 249
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                                                        121
                                                                                               87 GQQIQTLSSKIVARNESLKQ---QARSAQKSNAATSYINAIINSKSVSDAINRVSA---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                    250 QEQAAQAQAQAANNNNT---QATDASDQQAAAADNTQ--AAQTG------DSTDQS 293
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY.
WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
"FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1999-110-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-110-09
NUMBER OF SEO ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
                                                        62 VAIWSEENGÖDDLKWYHASNDGSNQLTVHFNÄENHGSKVGSYIAHAYITYTDGNRVGVNL
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                      - AENORLEAOS
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                    60 GQVSALQTQQAELQ------
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LENGTH: 257
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Sequence 3, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
ITILE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
ITILE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
ITILE OF SOURCE 30853/40359A
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                                                                                                                                                                                      10.9%; Score 229; DB 7; Length 971; 26.4%; Pred. No. 3.3e-06; Live 65; Mismatches 159; Indels
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APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT PILLING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILLING DATE: 1999-03-19
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 1/3/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 971
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                                                                                                                                   ; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-3
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SOFTWARE: Patentin Ver. 2
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Best Local Similarity
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LENGTH: 1236
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                                                                              127 SKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQETIAQNT 186
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SAVLVSGVTLSSATTLSAIKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQ 66
                                                                                                                                                                                                                               67 TOQAELQAENORLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:| | : : | : : | : : | |:| | : : | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:
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APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Soster, Simon
APPLICANT: Soster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: PLOGESYMO
CURRENT PRILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SEQ ID NO 413
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; ORGANISM: Staphylococcus epidermidis
US-10-485-517-413
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Publication No. US20050256299A1
GENERAL INFORMATION:
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nes 73; Conservative
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Sequence 211, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:
GENERAL THORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US 11/052,554A

CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR RPLING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SEGTHARE: Patentin version 3.3

SEQ ID NO 211

LENGTH: 1562
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                                                                                                                                       68 GGKIGSTWGNANSWATAAQAAGFTVNNTPEEGAIMQSSEGAFGHVAFVESVNNDGSITVS 127
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                                                                                                             346 APWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQ 404
                                              20 GHTTHADAAE--NNNQQQST-----YNYSTTEVSF-SNSGNLYTSGQCTWYVDKT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 NAKNT------BIAAANEBIRKRNATAKABYETKLAQYQAELKRV-----QE
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                                                                                                                                                                                                         405 EANYAG 410
                                                                                                                                                                                                                                                       EMNYDG 133
                                                                                                                                                                                                                                                                                                                                                   US-11-052-554A-211
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187 STYWSDAKYWASNAANDGYQVDNTPSVGAIMQSTPGPYGHVAYVERINGDGSILISEMNY 246
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                                                                                                                                                                                        Sequence 1682, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY.
TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERBENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
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Publication No. US20050255478A1
GENERAL INFORMATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILLS REPRENCE: P19480U2
CURRENT APPLICATION NUMBER: US/10/793,626
PRIOR PILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SSEPTURE PARENTIN Ver. 2.1
SSEQ ID NO 2870
LENGTH: 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
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                                              409 AGNOSIGNYR 418
                                                                                         247 ANGPYNMNYR 256
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Matches 50; Conserv
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Best Local Similarity
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US-10-793-626-2870
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LENGTH: 149
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245

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ORGANISM: Artificial Sequence
                                                                                                                                           93; Conservative
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CRGANISM: Homo sapiens
US-10-821-234-901
                                                                      US-10-793-626-3154
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US-10-821-234-901
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             APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: RENELAND, RICHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: THEREOF
FILE REFREENCE: SEQ-4069-CP
CURRENT FILING DATE: 2004-05-28
PRIOR FILING DATE: 2003-11-25
PRIOR PELING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 496-2
NUMBER OF SEQ ID NOS: 496-2
NUMBER OF SEQ ID NOS: 496-2
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R---SEQQKATEKERVAQEKDQLQEQLQALKESLKVTKGSLEBEKRRAADA-----LE 730
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Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPRENCE: PU348003
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1999-111-09
PRIOR PLING DATE: 1999-111-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Mismatches 141; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 191.5; DB 6; Length 2101; 22.0%; Pred. No. 0.0011;
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Matches 90; Conservative
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US-10-857-780-23
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US-10-793-626-3154
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LENGTH: 1095
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Applicant, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US, 60/462,047
PRIOR APPLICATION NUMBER: US, 60/462,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 VAA------NOETIAQNTNA----LNTQQAQLEAAQLNLQ------AELTTA
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                              91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 ----AAQAVNNSD---QESTTATAAQPSASSASTAAVAANTSSANTYP 334
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                                                                                                                                                    Length 1095;
                                                                                                                                                    Query Match

8.9%; Score 187.5; DB 6; Length
Best Local Similarity 22.7%; Pred. No. 0.00088;
Matches 93; Conservative 59; Mismatches 166; Indels
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SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 901_
LENGTH: 1586
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1219 --HSLTQAKEESEKQLCLIE----AQTMEALLALLPELSVLAQQNYTEWLQDLKEKGPTL 1272
                                                            260 ANNNYTOATDASDQOAAADNTQAQTGDS-----TDQSAAQAVNNSDQESTT- 307
                                                                                       308 ----ATAAQPSASSASTAAVAANTSS 329
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Search completed: February 15, 2006, 18:35:23 Job time : 9.33977 secs

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February 15, 2006, 17:57:02; Search time 113.754 Seconds (without alignments) 1668.609 Million cell updates/sec
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1 MKKRILSAVLVSGVTLSSAT......SIGNYRGWFNPGSVSYIYPN 432
5.1.7
Biocceleration Ltd.
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GenCore version (c) 1993 - 2006
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Add93652 Streptoco	Adx37275 Streptoco	Add93651 Streptoco	Adx37274 Streptoco		Adx37273 Streptoco	Add93649 Streptoco	Adx37272 Streptoco	Aeb91500 Microbial	Add93653 Streptoco		Abp29684 Streptoco	Adu69524 S agalact	-	Adv81808 Streptoco	Adv79645 Streptoco	Aeb91542 Microbial	Abp25919 Streptoco	_	Abp25918 Streptoco	O3	Adt50226 S pneumon	Adt50165 S_pneumon	Adr94595 Novel S.
SUMMARIES	ΩI	ADD93652	ADX37275	ADD93651	ADX37274	ADD93650	ADX37273	ADD93649	ADX37272	AEB91500	ADD93653	ADX37276	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645	AEB91542	ABP25919	ADR83884	ABP25918	ABU02747	ADT50226	ADT50165	ADR94595
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AEA58465 ADK47859 ADK785027 AAR14150 AAR14150 AAR129734 ABU29734 ABU29734 ABU29734 ABU29734 AAY00250 ABP43469 ABP43469 ABP43469 ABP43469 ABP43469 ABP43469 ABP43469 ABP43469	ADV00251 ABP43470 ABU88498
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22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 2 6 4 3 2

## ALIGNMENTS

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B. ADD93652 standard; protein; 432 AA. 07-MAR-2002; 2002US-0363209P. 07-MAR-2003; 2003WO-US006962. (first entry) Taubman MA; (FORS-) FORSYTH INST. Streptococcus mutans. WPI; 2003-845091/78. GENBANK; AY046413. WO2003075845-A2. 29-JAN-2004 18-SEP-2003. Smith DJ, ADD93652; RESULT 1 ADD93652 

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 5; Page 8; 49pp; English.

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Dispitopic or multiplications production of an antibody in a mammal. Dispitopic or multiplication peptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in

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New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                 The invention relates to a composition comprising a fragment of a gluca binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                             Score 2116; DB 9
Pred. No. 8e-135;
; Mismatches 0
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                                                                              Claim 3; SEQ ID NO 32; 73pp; English
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 432; Conservative
         2005-151644/16
                                                                                                                                                                          Sequence 432 AA;
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                                                                                MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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microparticle; major histocompatibility complex; tooth disease.
                                        Length 432;
                                                             Indels
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                                      100.0%; Score 2116; DB 7;
100.0%; Pred. No. 8e-135;
ive 0; Mismatches 0;
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99US-0115142P.
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2002US-0363209P.
2002US-0402483P.
2003US-00383930.
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passive immunisation.
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(TAUB/) TAUBMAN M A.
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                                                  Similarity
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08-JAN-1999;
12-APR-1999;
07-MAR-2002;
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Length 432;
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The present sequence is the protein sequence of the glucan binding protein—B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, cowplently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipitopic polypeptides can be prepared synthetically or by recombinant bNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                                                         composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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Pred. No. 1.1e-133;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                          Claim 5; Page 8; 49pp; English
              07-MAR-2003; 2003WO-US006962.
                                              07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
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99.3%;
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Matches 429; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
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                                                                                                                 immunogenicity, immune stimulation, glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                      Streptococcus mutant glucan binding protein B variant #3
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ADX37274 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microparticle, useful for prod
mammals against dental caries.
                                                                                                                                                                                                                                                                                               08-JAN-1999; 99US-01151422
12-ARR-1999; 99US-00290049
07-MAR-2002; 2002US-045482P
08-AUG-2002; 2002US-0402483P
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                             Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                   SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                     ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGOIOVOBANYAGNOSIGNYRGW
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Pred. No. 5.1e-132;
1; Mismatches 3;
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                                                                                                                                                                                            ADD93650 standard; protein; 431 AA
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                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2003; 2003WO-US006962.
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08-AUG-2002; 2002US-0402483P.
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98.8%;
                                                                                                        432
                                                                                                                     Taubman MA;
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MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG

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Best Local Similarity 98.8 Matches 427; Conservative

Local Similarity

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                                                                                                                                                                                                                                                                                          241 KAAAEAKALQEQAAQAAA-NNNTQATDASDQQAAAADNTQAAQTGBSTEQSAAQAVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE
                                                                                                                                                                    181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAAA
                                                                                                                                                                                                                                                    KAAAEAKALOEOAAOAAAANNNNTOATDASDOOAAAADNTOAAOTGDSTDOSAAQAVNN
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                                                                                    TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAAT
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microparticle; major histocompatibility complex; tooth disease.
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08-JAN-1999; 99US-015542P.
12-ARR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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TAUBMAN M A.
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (FHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipatiopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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  "HLA-binding peptide"
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08-AUG-2002; 2002US-0402483P.
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289. .308
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Best Local Similarity
Matches 426; Conserv
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protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                   181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAQAAAEA
                                                                                                                                       1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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:e= "HLA-binding peptide"
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113. .132
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                                                                        Score 2074.5;
Pred. No. 5.1e
1; Mismatches

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    /note= "HLA-binding"

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                                                                                    Best Local Similarity 98.8
Matches 427; Conservative
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                                                                                                                                                                      MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds Streptococous mutans GpbB protein of the invention.
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                                                                                                         Score 2070.5; DB 9; Length 431;
Pred. No. 9.5e-132;
1; Mismatches 4; Indels 1;
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2004US-0589227P.
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                                                                                 TIAQNTNALINTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAGAAAQAAABA
                           QVSALQTQQAELQAESQVELEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
                                                                                                                                                                                        KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
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      QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
                                                                INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE
                                                                                                                              TIAONTNALNTOOAOLEAAOLNLOAELTTAODOKATLVAOKAAAEEAAROAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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08-JAN 1999; 99US-0115142P.
12-APR-1999; 99US-00250049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-0403493P.
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(TAUB/) TAUBMAN M A.
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dentifying adhesin and adhesin. The proteins, by computing the sequencebased attributes of protein sequences using five attribute modules of a
neural network software, training an artificial neural network (ANN) for
each of the computed five attributes, and identifying the adhesin and
adhesin-like proteins having probability of being an adhesin (Pad) as
equal or greater than 0.51. Also claimed is a set of 274 annotated genes
encoding adhesin and adhesin-like proteins, having 105 fully
genes encoding adhesin-like proteins, having 105 fully
cefined 306-15876 base pairs (SEQ ID NO: 659-763), a set of 279 annotated
adhesin and adhesin-like proteins, having 105 fully
conditions and adhesin-like proteins, having 105 fully
conditions and adhesin-like proteins, having 105 fully
sequences; a set of 279 annotated
adhesin and adhesin-like proteins, having 105 fully defined 53-3716 base
conditions, having 105 fully defined 106-5291 base pair (SEQ ID NO:
280-384) sequences; and a fully connected multilayer feed forward ANN (1)
based on (M1). (M1) is useful for identifying adhesin and adhesin-like
proteins for therapeutic potential, and identifying and short-listing
proteins for further testing in development of new vaccine formulations
to eliminate diseases caused by various pathogenic organisms. (M1) is Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network. present invention relates to a computational method (M1) for Claim 16; SEQ ID NO 210; 402pp; English 

Sequence 431 AA;

protein sequence.

useful for identifying putative adhesins that are important in drug discovery and preventing therapeutics for whooping cough, pneumonia, gastric ulcer and urinary tract infections. (M1) identifies adhesins from distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin

120 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120 9 9 1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVVTIQG QVSALQTQQABLQABRQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY Gaps 1; DB 9; Length 431; 4; Indels Score 2070.5; DB 9 Pred. No. 9.5e-132; 1; Mismatches 4; 97.8%; 98.6%; Best Local Similarity 98.6 Matches 426; Conservative 61 Query Match 61 유 g ò ò

121 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180

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KAAAEAKALQEQAAQAQAAA-NNNTQATDVSDQQAAADNTQAAQTGDSTEQSAAQAVNN 299 KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN SDOESTTATAAQPSASSASTAAVAANTSSANTYPAGOCTWGVKSLAPWVGNYWGNGGGWA 241 241 301

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360

Ź ADD93653 standard; protein; 431 29-JAN-2004 ADD93653; ADD93653 

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.

Streptococcus mutans glucan binding protein-B.

Streptococcus mutans.

WO2003075845-A2

18-SEP-2003,

07-MAR-2003; 2003WO-US006962.

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Smith DJ, Taubman MA;

2003-845091/78. GENBANK; AY046414. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 5; Page 8-9; 49pp; English.

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 5SM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibity complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiplicytopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.

Sequence 431 AA;

Gaps 1; Length 431; Indels 5. Score 2066.5; DB 7 Pred. No. 1.8e-131; 1; Mismatches 5; 98.48; Local Similarity 98.4 nes 425; Conservative Query Match Best Loca Matches

1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising a fragment of a glucan binding protein-B (GDBB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
            KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN
                                        SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
                                                                                                                                                                                                                                                                                     immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                 Streptococcus mutant glucan binding protein B variant
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08-JAN 1999; 99US-0115142P.
12-APR-1999; 99US-002500049.
07-MAR-2002; 2002US-0163209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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(TAUB/) TAUBMAN M A.
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DB 9; Length 431; 5; Indels

Score 2066.5; DB 9; Pred. No. 1.8e-131; 1; Mismatches 5;

97.7%;

Matches 425; Conservative

Similarity

Query Match Local 1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG

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                                                                                                                                                                                                                                                                                                        121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQGENQAAINTVAANQE
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ASAAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
                                                                                                              QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
                                                                                                                                                       TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAA
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07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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(GENO-) INST GENOMIC RES
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N-PSDB; ABN70315.
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etreptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or disagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy, Antibodies to (1) are used for affinity when the composition when the composition are used for affinity the disease caused by the used in gene therapy. Antibodies to (1) are used for affinity and may be the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of the distribution of
invention relates to a protein (ABP25413-ABP30895) from group B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus proteins
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                                                                                                    QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                                                                    KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300
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                                                                  TIAONTNALNTOQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAA
                                                                                                                                                                                                                  1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                                                           SDQ---ESTTATA----AQPSASSASTAA------VAANTSSANTYPAG
                           Gaps
                          45;
 DB 5; Length 447;
                          99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             395 GV-OGGOIOVOEANYAGNOSIGNYRGWFNP---GSVSYIYPN 432
                                                                                                                                                                                                                                                                                                                                                                                                                             SVANNSSIQVMESNYAGNMSIGNYRGSFNPSASGSVYYIYPN 447
58.1%; Score 1229.5; DB 59.7%; Pred. No. 7.9e-75
                         42; Mismatches
                         Matches 276; Conservative
             Local Similarity
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immune stimulation; antigen; bacterial surface display; hyperimmune serum reactive antigen; vaccine; bacterial infection; antibacterial; infection.
                                                                                                  S agalactiae hyperimmune serum reactive antigen segid 219.
                        ADU69524 standard; protein; 447 AA
                                                                         10-FEB-2005 (first entry)
                                                                                                                                                                          Streptococcus agalactiae
                                                 ADU69524;
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vector; a hyperimmune serum-reactive antigen comprising the vector; a hyperimmune serum-reactive antigens of vector; a hyperimmune serum-reactive antigens of consisting of e.g., 85, 299, 467 cor 812 amino acids; fragments of hyperimmune serum-reactive antigens antigens of process for producing a Streptococcus agalactiae hyperimmune serum cactive antigens. A process for producing a cell that expresses a S. agalactiae hyperimmune serum reactive antigen; a process for producing a cell that expresses a S. agalactiae hyperimmune serum reactive antigen; a pharmaceutical composition, especially a vaccine, comprising the hyperimmune serum-reactive antigen; a mutaleic acid molecule; an antibody that binds at creative antigen or nucleic acid molecule; an antibody that binds at cleast to a selective part of the hyperimmune serum-reactive antigen; a method for identifying an antigonist that binds to the hyperimmune serum-reactive antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an antigen; a method for identifying an interactive antigen; and a process for in vitro diagnosing a disease related to expression of the hyperimmune serum reactive antigen; and a process for in vitro diagnosing of the hyperimmune serum reactive antigen; and a process for in vitro diagnosing a disease related for isolating, purifying and/or identifying an interaction partner of the hyperimmune serum creactive antigen; and/or identifying to the hyperimmune serum reactive antigen is useful for isolating of the hyperimmune serum creactive antigen; or the hyperimmune serum reactive antigen; or the hyper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment. Also described are: a vector comprising the nucleic acid molecule; a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding a hyperimmune serum reactive antigen, useful for the manufacture of a vaccine against Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              functional nucleic acid comprising aptamers or spiegelmers. The nucleic acid molecule is useful for the manufacture of a functional ribonucleic acid comprising ribozymes, antisense nucleic acids or siRNA. The nucleic acid molecule, hyperimmune serum-reactive antigen or antibody is useful for the manufacture of a vaccine against S. agalactiae infection. This is the amino acid sequence of a Streptococcus agalactiae hyperimmune serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKRILSAVLVSGVTLGTAAV--TVNADDFDSKIAATDSVINTLSGQQAAAQNQVTAIKG
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                                                                                                                                                                                                                                                                                            Kallenda S,
                                                                                                                                                                                                                                                                                            Horky M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; SEQ ID NO 219; 221pp; English
                                                                                                                                                                                                                                                                                            Hanner M,
                                                                                                  06-MAY-2004; 2004WO-EP004856.
                                                                                                                                                                                    28-NOV-2003; 2003EP-00450266
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                                                                                                                                                                                                                                       (INTE-) INTERCELL AG.
                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-821662/81.
                                                                                                                                                                                                                                                                                          Meinke A, Nagy E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reactive antigen.
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                                                                                                                                                        07-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection
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Zouine M,
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INTILINSKSVSDAVNRVVAIREVVSANEKMLAQQEADKAALEAKQIENQNAINTVAANKQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
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Poyart C, Trieu CP, Ku
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                                                                                                                                                                                                                       SDQ---ESTTATA-----AQPSASSASTAA----
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Couve E, Buchrieser C,
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                    Gaps
equivalent for the present basic patent FR2824074A1. WO200292818A2 contains 6617 sequence whereas the present patent only contains 2344
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                                                                                                                                    Length 447;
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Poyart C, Trieu-Cuot
                                                                                                                                  58.1%; Score 1229.5; DB 8; Length 59.7%; Pred. No. 7.9e-75; ive 42; Mismatches 99; Indels
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Couve E, Buchrieser C,
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                                                                                                                                                               Local Similarity 59.7
les 276; Conservative
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The present invention relates to novel Streptococcus agalactiae
nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
novel polypeptides (II; ADV78999-ADV81205-ADV83340). The
nucleotide sequences encode polypeptides of S. agalactiae involved in the
nucleotide sequences encode polypeptides of S. agalactiae involved in the
synthesis of amino acids, cell membranes, intermediate (central)
cetabolism, energetic metabolism, fatty acid and phospholipid metabolism,
nucleotide metabolism including purinnes, pyrimidines and/or nucleosides,
regulatory functions, replication, transcription, translation, protein
regulatory functions related to transposons, biosynthesis of
and/or analogues, functions related to transposons, biosynthesis of
cofactors, prosthetic groups and transposters, cell membrane proteins and
cellular machinery. (I) are useful for the detection and/or amplification
of nucleic acids. Pharmaceutical composition comprising (I) or [II] are
useful for treatment of a bacterial S. agalactiae infection. The complete
genome of Streptococcus agalactiae is given in ADV81204. Note: The
present patent is an equivalent for the basic patent FR2824074Al, which
contains only 2344 sequences.
Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                                                                                                        Claim 6; SEQ ID NO 2949; 439pp; French.
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; Score 1229.5; DB 8; Length 447; ; Pred. No. 7.9e-75; 42; Mismatches 99; Indels 45; Gaps 58.1%; Best Local Similarity 59.74 Matches 276; Conservative

MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG 60 INAIINSKSVSDAINRVSAIREVVSANEKMIHQQEQDKAAVEQKHQENQAAINTVAANQE 180 TIAONTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240 -59 118 181 121 61 g a g 8 ò ò ઠે

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US-10-797-821-32 2116 1 MKKRILSAVLVSGVTLSSAT......SIGNYRGWFNPGSVSYIYPN 432 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB R Maximum DB R

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PIR 80:\*
1: pir1:\*
2: pir2:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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æ	Query Match	49.8	49.8	32.2	31.1	25.4	16.8	16.2	15.1	12.3	12.1	12.0	11.9	11.2	10.9	10.8	10.8	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.5	10.5	10.4	10.3	10.3	10.2
	Score		1053	681.5	658	537.5	356	343.5	319	259.5	256	254.5	251	237	230	228	228	226.5	226.5	226.5	226.5	226.5	225.5	225.5	222	221.5	221	$\overline{}$	217	215
	Result No.		7	e	4	S	ø	7	æ	Ø	10	11	12	13	14	15		17	18	19	20	21	22	23	24	25	26	27		29

120

120

09 9 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180

121

1 MKKKILASLLLSTVMVSQVAVLTTAHAETTDDKIAAQDNKISNLTAQQQEAQKQVDQIQE

рp ò g 8 8

1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQANTIQG

KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNN 300

241 241

181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240

360

301 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA 

8 8 8

KRASQQQSV-----LASANTNLTAQVQAVSESAAAPVRAKVRPT-

314

361 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRG 419

M6 protein - Strep	Htrl7 transducer [	FmtB protein [impo	cell surface antig	IgA-specific metal	probable secreted	IgA-specific metal	M protein precurso	regulatory protein	M protein precurso	IgG-binding protei	hypothetical prote	regulatory protein	LcKin kinesin-rela	IgA-specific metal	extracellular matr
A26297	D84325	D90011	A43607	A81937	T34852	S61314	S30284	S01272	A60115	S57835	G86865	A26639	A47334	C81169	T31110
7	~	~	N	7	N	~	7	~	N	7	N	~	7	0	0
483 2	536 2	2481 2	1566 2	1773 2	1156 2	1561 2	436 2	574 2	564 2	528 2	334 2	555 2	955 2	1815 2	2055 2
	10.0 536 2									9.5 528 2					
10.1		6.6	6.6	6.6	8.6	9.7	7.6	9.6	9.6		9.5	9.5	9.5	9.5	

## ALIGNMENTS

	RESULT 1
secreted 45 kd protein (imported) - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95258 R;Tettellin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He: on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 233, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Accession: G9528 A;Resference number: A95000; MUID:21357209; PMID:11463916 A;Residues: 1-324 cKURA A;Residues: 1-324 cKURA A;Residues: 1-324 cKURA A;Residues: 1-324 cKURA A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216 Query Match Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps	G95258
C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95258 R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He: on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a vinulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-392 kKUR> A;Status: Preferences: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE005672 A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216 Query Match C;Genetics: A;Gene: SP2216 Query Match Date: A; Mainlarity 49.8%; Score 1053; DB 2; Length 392; Best Local Similarity 49.8%; Marches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4;	secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95258 R;Tettelin, H: Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He: on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 233, 498-506, 2001 A;Authors: Loffus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atthors: Loffus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atthors: Loffus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atthors: Loffus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atthors: Loffus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: G95258 A;Accession: G9528 A;Accession: G9528 A;Residues: 1-392 <kur> A;Residues: Leferences: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPIO000051B81; GB:AE005672 A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216 Query Match A;Gene: SP2216 Query Match Macches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps</kur>	C;Species: Streptococcus pneumoniae
C;Accession: G95258 R;Tettellin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heron, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Residues: 1-324 xCMP A;Residues: L-324 xCMP A;Residues: L-324 xCMP A;Residues: L-324 xCMP A;Gene: SP2216 A;Experimental source: strain TIGR4 C;Genetics: A;Genetics: A;Gene: SP2216 Ouery Match Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps	C;Date: 03-Aug-2001 #sequence revision 03-Aug-2001 #text_change 09-Jul-2004
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He; On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a vinulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; WUID:21357209; PMID:11463916 A;Accession: G95258 A;Scatus: Preliminary A;Molecule type: DA A;Residues: 1-392 cKUR> A;Residues: 1-392 cKUR> A;Residues: 1-392 cKUR> A;Residues: 1-392 cKUR> A;Residues: 1-392 cKUR> A;Residues: 1-392 cKUR> A;Gross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE005672 A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216 Query Match Macches: 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches: 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4;	C;Accession: G95258
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Bon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 233, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: G95258 A;Accession: G95258 A;Accession: G95258 A;Accession: G95258 A;Residues: 1-92 <kur> A;Residues: 1-92 <kur> A;Residues: 1-92 <kur> A;Residues: 1-92 <kur> A;Residues: 1-92 <kur> A;Gross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE005672 A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216 Query Match Query Match Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps</kur></kur></kur></kur></kur>	R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidt
nson, T.; Hickey, E.K.; Holt, I.E. Science 233, 499-566, 2001 A;Authors: Loftus, B.J.; Wang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Atthors: Loftus, B.J.; Wang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Attle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Accession: G9528 A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Residus (99528 A;Residus 1-392 «KUR> A;Residues: 1-392 «KUR> A;Residues: 1-392 «KUR> A;Residues: 1-392 «KUR> A;Experimental source: strain TIGR4 C;Genetics: A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216 Query Match Query Match Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps	on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I,
Science 293, 498-506, 2001  A,Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A,Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A,Racesaton: G95258 A,Accesation: G95258 A,Scatus: preliminary A,Molecule type: DNA A,Residues: 1-392 <kur> A,Residues: 1-392 <kur> A,Experimental source: strain TIGR4 C,Genetics: A,Experimental source: strain TIGR4 C,Genetics: A,Gene: SP2216 Query Match Genetics: A,Gene: G17; Conservative 74; Mismatches 93; Indels 52; Gaps 4; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4;</kur></kur>	nson, T.; Hickey, E.K.; Holt, I.E.
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A;Recession: G95258 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 1-392 <kur> A;Residues: 10N1PROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPIO00051B81; GB:AE005672 A;Residues: SP2216 A;Genetics: A;Gene: SP2216 A;Genetics: A;Genetics: A;Gene: SP2216 A;Genetics: A;Gene: SP2216 A;Genetics:</kur></kur></kur></kur></kur></kur></kur></kur></kur>	Science 293, 498-506, 2001
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A; Reference number: A95000; MUID:21357209; PMID:11463916 A; Accession: G9528 A; Accession: G9528 A; Accession: G9528 A; Residues: 1-392 * KURA A; Residues: 1-392 * KURA A; Residues: 1-392 * KURA A; Coss-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE005672 A; Experimental source: strain TIGR4 C; Genetics: A; Gene: SP2216 Query Match Query Match Best Local Similarity 49.8%; Score 1053; DB 2; Length 392; Best Local Similarity 49.8%; Pred. No. 2.3e-45; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4;	A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Accession: G95258 A; Status: preliminary A; Accession: G95258 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-392 «KUR> A; Residues: 1-392 «KUR> A; Residues: 1-392 «KUR> A; A; Cross-references: UNIPROT: Q97N55; UNIPROT: Q8DMY4; UNIPARC; UPIO000051B81; GB: AE005672 A; Experimental source: strain TIGR4 C; Genetics: A; Gene: SP2216 Query Match Query Match Beat Local Similarity 49.8%; Score 1053; DB 2; Length 392; Beat Local Similarity 49.8%; Proced. No. 2.3e-45; Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4;	A; Reference number: A95000; MUID: 21357209; PMID: 11463916
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49.8%; Score 1053; DB 2; Length 392; Similarity 49.8%; Pred. No. 2.3e-45; 7; Conservative 74; Mismatches 93; Indels 52; Gaps	A;Gene: SP2216
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	Matches 217; Conservative 74; Mismatches 93; Indels 52; Gaps 4;

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C.Species: Streethcoccus pneumoniae
C.Bate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C.Accession: B98124
R.Hoskins, J.A., Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; J. Bacteriol. 183, 5709-5717, 2001
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A.Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE007317; C;Genetics:
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C;Species: Lactococcus lactis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JN0097
R;Van Asseldonk, M.; Rutten, G.; Oteman, M.; Siezen, R.J.; de Vos, W.M.; Simons,
Gene 95, 155-160, 1990
                                                                                                                                                 general stress protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6)
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TSAAAAGFRTGSTPQVGAIACWNDGGYGHVAVVTAVESTTRIQVSESNYAGNRTIGNHRG 374
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49.8%; Score 1053; DB 2;
Best Local Similarity 49.8%; Pred. No. 2.3e-45;
Matches 217; Conservative 74; Mismatches 93;
                                WFNP----GSVSYIY 430
                                                               WFNPTTTSEGFVTYIY 390
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A;Molecule type: DNA
A;Residues: 1-392 <KUR>
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Pypothetical protein usp45 [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis Lactococcus L86003 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001 A;Fitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A;Fitle: R8603 A;Fitle: R8603 A;Status: preliminary A;Status: preliminary A;Molecule type: DNA.
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A;Cross-references: UNIPROT:Q9CDJ1; UNIPARC:UPI0000C6BFC; GB:AE005176; PID:g12725296; P)
A;Experimental source: strain IL1403
C;Genetics:
A,Title: Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis. A,Reference number: JN0097; MUID:91071599; PMID:2123812
A,Accession: JN0097
A,Status: preliminary
A,Status: preliminary
A,Residues: 1.461 < VAN>
A,Residues: 1.461 < VAN>
A,Coos-references: UNIPARC:UP1000016D72B; GB:M35374
                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 PAGQCT---WG-----VKSLAPWVGNYWGNGGQWAASAAAAG--YRVGSTPSAGAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 V-----WNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRGWFNPGSVSYIYP
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                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                               Query Match 32.2%; Score 681.5; DB 2; Best Local Similarity 35.6%; Pred. No. 6.1e-27; Matches 171; Conservative 105; Mismatches 136;
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Db 301 NSSTGSSSTESSTVPESSTQBSTPANTESSSSSNTNVNNNTNNSTNNSTNNSTT 360  Qy 333YPAGQCTWGVKSLAPWVGNYWGNG 356  Db 361 NNNNNNTVTPAPTPTPTPAPAPAPNPSGSVNGAAIVAEAYKYIGTPYVWGKDPSG 417  Qy 357	SULT 6  1763  pridoglycan lytic protein P45 [imported]  Species: Listeria innocua Date: 27-Nov-2001 #sequence_revision 27-N  Accession: AC1763  Jasser, P.; Frangeul, L.; Buchrieser, C.; Jones, L.M.; Karst, U.  Jones, L.M.; Karst, U.  Authors: Kreft, J.; Kuhn, M.; Kunst, F.;  C.; Schlueter, T.; Simoes, N.; Tierrez,  Title: Comparative genomics of Listeria s  Reference number: AB1077; MUID:21537279;  Accession: AC1763  Status: preliminary  Accession: AC1763  Scholecule type: DNA  Residues: 1-398 AGLA>  Cross-references: UNIPROT:Q92778; UNIPARC  Sarperimental source: strain Cliph11262  Senetics:	00.ery Match   16.8%; Score 356; DB 2; Length 398; Best Local Similarity   27.1%; Pred. No. 6.2e-11;   0.0cal Similarity   27.1%;   0.0cal Similarity   27.1%;   0.0cal Similarity   0.0
	; > 0 12—12   F 4 4 4 5 6 7	R; Fueret, P.; Moecch, H.U.; Solloz, M.  Nucleic Acids Res. 17, 6724, 1989  A; Title: A protein of unusual composition from Enterococcus faccium.  A; Accession: 805542; MuID: 89985998; PMID: 2780297  A; Accession: 805542  A; Moeccule type: DNA  A; Moeccule type: DNA  A; Concentration: 505542; MuID: 89985998; PMID: 2780297  A; Corse-reference number: 805542; MuID: 89985998; PMID: 2780297  A; Corse-reference: UNIPPOT: P1562; UNIPARC: UPI000016F6FC; GB: X16421; EMBL: M26048; NID: SA; Corse-reference: UNIPPOT: P1562; UNIPARC: UPI000016F6FC; GB: X16421; EMBL: M26048; NID: SA; Corse-reference: UNIPPOT: P1562; UNIPARC: UPI000016F6FC; GB: X16421; EMBL: M26048; NID: SA; Corse-reference: UNIPPOT: P15629; MISSIALA SOCKED S37.5; DB 2; Length 507;  Best Local S; Millarity 28.7%; Pred. No. 8.78-20;  Matches 146; Conservative 89; Mismatches 172; Indels 101; Gaps 12;  MISSIALANVSSPIAAADDPDSOQOMANADAQOAAQAQANTIQQOSALOTQO 69  10 LVSGVTLSSATTLSAVKADDPDSOQOMANADAQOAAQAQANTINKA 60  CON TO AELQAENORLEAGAATLCQOLOGENERICANDANOAAQASOSOIELLEGOVANINKA 60  CON TO AELQAENORLEAGAATLCQOLOGENERICANDANOACASONINANDANOETIAONADA 235  11 LADAVGRIQAMSTIVKANQDLVQQCKEDKQAVEAKABNEAKQAELDANQAALESQARGDL 180  CON TOO ADAINKVARIREVARANADADAOAAANTRXAAABABAAAQAANAAAAAAAAAAAAAAAAAAAAAAAAAA

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12.3%; Score 259.5;
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Patisary Deptidoglycan lytic protein P45 [imported] - Listeria monocytogenes (strain EGD-e) C; Species: Listeria monocytogenes (c; Species: Listeria monocytogenes (c; Species: Listeria monocytogenes (c; Species: Listeria monocytogenes (c; Species: 27-Nov-2001 #text_change 09-Jul-2004 (c; Species: Jul-2004 alias) (c; Species: Jul-2004 alias) (d; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Joneinguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 alias, Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Reference number: Aliasoparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669 alias, John John A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA, A; Residues: 1-401 cGLAA,
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F70031
R;Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Entrich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Gect, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portefelle
B; Park, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffne, F.; Sekiguchi, J.; Sekowska, A.; Tosato, V.; Uchiyama,
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:Q9RE04, UNIPARC:UPI0000D019D, GB:NC_003210, PIDN:CAD00583.1
A,Experimental source: strain EGD-e
C;Genetics:
A,Gene: spl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 343.5; DB 2; Length (26.4%; Pred. No. 2.6e-10; tive 92; Mismatches 148; Indels
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Matches 111; Conservative
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. Ajauthors: Yoshikawa, H.; Zumstein, B.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A6580; MUID:98044033; PMID:9384377
A;Accession: F70031
A;Actaus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-473 <KUN>
A;Residues: 1-473 <KUN>
A;Cross-references: UNIPROT:P40767; UNIPARC:UPI0000060ABI; GB:Z99121; GB:AL009126; NID:g;A;Genetics:
A;Experimental source: strain 168
C;Genetics:
A;Genetics:
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A;Residues: 1-581 <WHI>
A;Cross-references: UNIPROT:Q9RU45; UNIPARC;UPI00000C195A; GB:AE001998; GB:AE000513; NID:
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1549
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T.; Zalewski,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKRILSAVLVSGVTLSS-----ATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQ 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.1%; Score 319; DB 2; Length 47 Best Local Similarity 23.9%; Pred. No. 5.1e-09; Matches 111; Conservative 94; Mismatches 187; Indels
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C;Accession: AH1387

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, B;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: DNA
A.Molecule: 1-436 kGLA>
A.Crose-references: UNIPROT: Q8Y4E2; UNIPARC: UPI0000055221; GB:NC_003210; PIDN: CAD00582.1;
A.Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wall binding proteins homolog lmo2504 [imported] - Listeria monocytogenes (strain
                                                                                                                                                                                            318
   ----EQDRGILE-AHIEDHRLL.----EEAKAQVEEKLETLEGHLVELE-NLMAQLEEQ 210
                                                                                                                                                                                                                                                            313
                                                                                                                                                                                                                                                                                                                        STAAVAANTSSANTYPA-----GQCT---WGVKSLAPWVGNYWGNGGQWAASAAAG 367
                                                                                                                                                                                                                                                                                                                                                                 314 ETGSVPSSSGSGFMRPATGDISSPFGYRTHPVTGQRKLHAGIDIRRGNRSNVPVVAAYDG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 TVVQST-----YSSGGYGNMVIIAHSYNGRQVTTLYAHLETRSVSAGQRVSKGQTIG 425
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C,Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C,Accession: AH1387
                                                                                                                  211 QKEKEKYMGELASREDELHGDLESLENDEBLLRQQEKALQEEYELWKKQEEERKAA----
                                                                                                                                                                                                                                        267 EKAAAEAAAQQAQAS -----SGGGGGSSNSDSGSNSGTTSRSNGGSSGGGG
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                                                               211 QDQKATLVAQKAAAEEAARQAAAQAAAEAKAAAEAKALQE-----QAAQAQAAANNN
                                                                                                                                                                                        264 NTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNNSDQESTTATAAQPSASSA----
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12.0%; Score 254.5; DB 2;
Best Local Similarity 23.0%; Pred. No. 7.1e-06;
Matches 97; Conservative 86; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 ----TGVQGG---QIQVQEANYAGNQSIGNYRGWFN 422
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H84099
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84099
A;Accession: H94099
A;Accession: H94099
A;Coust preliminary
A;Molecule type: DNA
A;Coust references: UNIPROT:Q9K6X4; UNIPARC:UPI0000C424C; GB:AP001519; GB:BA000004; NID
A;Coust references: UNIPROT: C9K6X4; UNIPARC:UPI0000C424C; GB:AP001519; GB:BA000004; NID
A;Gene: BH3600
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H84099
cell wall-binding protein BH3600 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                          62 VSALQTQQAELQAENQRLEAQSATLGQ---QIQTLSSKIVARNESLKQQARSAQKS---N 115
                                                                                                                                                                                                                                                                  116 AATSYINAIINSKSVSDAINRVSAIREVVSANEKMLHQ--------QEQDKAAV 161
                                                                                                                                                                                                                                                                                                                                                                                           213 RGLQGEQQTKLAELRDRRTRQADALAELQRSAQGQQAVAVRTQAQQALTAQTIDSLVGNV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LTTAODOXATLVA-- 219
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                                                                                                                                             61
                                                                                                 16 LSSATTLSAVKADDPDAQIASQ------DSKINNLTAQQQAAQAQVNTIQGQ
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                                    Indels 149;
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; Pred. No. 5.5e-06; 67; Mismatches 176;
24.6%;
   Best Local Similarity 24.6
Matches 128; Conservative
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Best Local Similarity
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Query Match
Best Local Similarity 29.0°
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1763
C;Accession: AB1763
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, B49-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                               cell wall binding protein homolog lin2647 [imported] - Listeria innocua (strain Clip1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:0927Y9; UNIPARC:UPI0000CC934; GB:AL592022; PIDN:CAC97874.1;
A,Experimental source: strain Clip11262
                                                      323 PVTGKYESHKGQDIAGGGTVTVSAAASGTVVFSGFGASGSGF---GGYGYVVKIDHGNGF 379
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---GGQWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 QQAA---QAQVNTIQGQVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 KQQARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDK---AAV 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 QCTWGVKSLA-PWVGNYWGN-----GGQWAASAAAAGYRV----GSTPSAGAVAVWND 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i Score 251; DB 2; Length 437;
i Pred. No. 1.1e-05;
80; Mismatches 149; Indels 106;
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B75310
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
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PWVGNYWGN-
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A;Molecule type: DNA
A;Residues: 1-437 <GLA>
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A; Gene: lin2647
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A;Experimental source: strain R1
C;Genetics:
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                                                                                                                                                           J.D.; Dodson,
T.; Zalewski,
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75310
C;Accession: B75310
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
S.; Smith, H.O.; Venter, J.C.; Praser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans 1
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B73310
A;Retsus: preliminary
A;Residues: 1-528 cWHI>
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139 AIREVVSANEKMLHQQEQDKAAVEQKHQENQAAIN-TVAANQETIAQNT-NALNTQQAQL 196
                                                                                                                                                                                                                                                       257 QAAANNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNNSDQESTTATAAQPSAS 316
                                                                                                                                                                                                                                                                                                                                                                   79 LEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVS 138
                                                                                                                                                                                                                                                                                               331 ASSÁSTATTKÁGEÁTEÓASÁÁASSASÁÁKTSETN----ÁKÁSETSAESSKTÁ----AAS 381
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                                       181 TEA-----SKSAAAAESSKSAAATSAGA-AKTSETNAAVSQQSAA----TS
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Job time : 22.0162 secs
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A;Cross-references: UNIPARC:UP10000137105; GB:AE000177; GB:U00096; NID:g1786955; PIDN:AA
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain i Sispecies: Bacherichia coli (Species: Bacherichia coli (Species: Bacherichia coli (Species: Bacherichia coli (Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 (Speciession: B90835 (Speciession: B90835) (Speciession: B90835) (Speciession: B90835) (Speciession: B90835) (Speciession: B90835) (Speciession: B90835) (Speciession: Bacherichia coli O157:H7 and gename sequence of enterohemorrhagic Escherichia coli O157:H7 and gename B90835)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKQ-QARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QKHQENQAAI--NTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL-TTAQDQKATLV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AOKKAEAAAALKKKAEAAEAAAEARKKAATEAAEKAKAEAEKKAAAEKAAADKKA--A 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 ELSSGKNAPKTGGGAKGNNASPAGSGNTKNNGASGADINNYAGQIKSAIESKFYDASSYA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 AAADNTQAAQTGDSTDQSAAQAVNNSDQESTTATAAQ-PSASSASTAAVAANTSSANTYP 334
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                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                     10.9%; Score 230; DB 2; Length 421; 28.5%; Pred. No. 0.00011; Live 65; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 228; DB 2; Length 971; 26.4%; Pred. No. 0.00034;
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                                                           C,Genetics:
A,Gene: tolA
A,Map position: 17 min
A,Start codon: GTG
C,Keywords: nucleotide binding; P-loop; transmembrane protein
E,14-34/Domain: transmembrane #status predicted <MSS>
F,78-301/Domain: helical #status predicted <HSR>
F,78-362/Region: nucleotide-binding motif A (P-loop)
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Best Local Similarity 28.5%
Matches 117; Conservative
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A;Molecule type: DNA
A;Residues: 1-971 <HAY>
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C;Genetics:
A;Gene: EC81650
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Carralle-3SN1;

MEDLINE-21481971; PubMed=11598068;

MEDLINE-21481971; PubMed=11598068;

Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,

Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,

Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding recoluting of the Streptococcus mutans gene encoding glucan binding recoluting and analysis of genetic diversity and protein production in the fort. Immun. 69:6911-6941(2001).

RMBL; ARO44413; AAK94503.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

RR InterPro; IPR007921; CHAP.

RR PRINTS; PR01852; SIBAPROTEIN.

RR PRINTS; PR01852; SIBAPROTEIN.

RR CAUSTIE; PS50911; CHAP. 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
Streptococcus mutans.
Bacteria, Firmicutes; Lactobacillales; Streptococcaeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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                                                              0501377 - STRTII
08E3F4 - STRA3
08D774 - STRA5
092778 - LISIN
0711WS3 - LISIN
0911WS3 - LISIN
0911W2 - BACCH
0731DG0 - BACCH
06M552 - CORGL
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   TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAAA
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                                        TIAQNTNALNITQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA
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Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by
differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
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"Cloning of the Streptococcus mutans gene encoding glucan binding
protein B and analysis of genetic diversity and protein production in
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DOI=10.1128/IAI.69.11.6887-6998.2001;
DOI=10.1128/IAI.69.11.6887-6998.2001;
"A 60-kilodalton immunodominant glycoprotein is essential for cell wall integrity and the maintenance of cell shape in Streptococcus
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n S., Duncan M.J., Taubman M.A., Smith D.J.;
loning of the gbpB gene from Streptococcus mutans.";
Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GS-5;
MEDLINE=21153617; PubMed=11254612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNPGSVSYIYPN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNPGSVSYIYPN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9AG98_STRMU PRELIMINARY;
Q9AG98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates."

Infect. Immun. 69:691-6941(2001).

EMBL, AV046412, AAV9452.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J., Duncan M.J.;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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Pred. No. 6.1e-88;
1; Mismatches 2;
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Q938V2;
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Matches 429; Conservative
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121 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TI AQNTNALNTOCACLEAAQLNLOAELTTAODOKATLVACKAAAEEAARQAAAAAAAEA
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STRAIN=UAIS9 / ATC 700610 / Serotype c;

STRAIN=LAIS9 / ATC 700610 / Serotype c;

MEDILINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;

Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Ajdic D.J., McShan W.M., Tanghin R.E., Savic G., Chang J.,

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Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Persengen R., Lis, Chu H., Najar F.Z., Lai H., White J., Roe B.A.,

Ferretti J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match

97.8%; Score 2070.5; DB 2; Length 431;
Best Local Similarity 98.6%; Pred. No. 1.2e-86;
Matches 426; Conservative 1; Mismatches 4; Indels 1;
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D Q8DWM3_TRMU PRELIMINARY; PRT; 431 AA.
AC Q8DWM37_
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative secreted antigen GbpB/SagA; putative peptidoglycan
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                               44620 MW; 464FE3B563FB7E51 CRC64;
                                                                                       EMBL, AX046410; AAK94500.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
PEam; PF05257; CHAP; 1.
PRINTS; PR01862; SIBARPOTEIN.
PROSTITE; PSC911; CHAP; 1.
SEQUENCE 431 AA; 44620 MW; 464FE3BS63FB
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NCBI_TaxID=1309;
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
Duncan M.J.;
                                                                                                                                                                                                                                                                                                                                                      Score 2074.5; DB 2; Length
Pred. No. 7.9e-87;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                             44592 MW; 3EBE21FC5E47232E CRC64;
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Last annotation update)
                       Infect. Immun. 69:6931-6941(2001).
EMBL; AF338445; AAK08104.1; -; Genomic_DNA.
EMBL; AY046411; AX045501.1; -; Genomic_DNA.
InterPro; IPR070321; CHAP.
InterPro; IPR070348; SibA.
Pfam; PF05557; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS55931; CHAP; 1.
SEQUENCE 431 AA; 44592 MW; JEBE21FC5E47232
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Q938V3;
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 98.8
Matches 427; Conservative
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NCBI_TaxID=1309;
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"Identification and molecular analysis of PcsB, a protein required for cell wall separation of group B streptococcus.";
J. Bacteriol. 183:1175-1183(2001).
EMBL; AJ77292; CAC28144.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
     protein B and analysis of genetic diversity and protein production in calinical isolates.",
Infect. Immun. 69:6931-6941(2001).
EMBL; AY046414; AAK94504.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PP05257; CHAP; 1.
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MEDLINE=21101799; PubMed=11157929;
DOI=10.1128/JB.183.4.1175-1183.2001;
Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
                                                                                                                                                                                                                                                                                           97.7%; Score 2066.5; DB 2; Length 98.4%; Pred. No. 1.8e-86; ive 1; Mismatches 5; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                          431 AA; 44650 MW; 05D38D8D8BC4609F CRC64;
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PROSITE; PS50911; CHAP; 1.
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Q9AKA4;
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Pred. No. 1.2e-86;
1; Mismatches 4; Indels 1;
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
Duncan M.J.;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                                                                                                                                                                                     2D1CA685248CCD3E CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
EMBL; AE014855; AAN57811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR00148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS0911; CHAP; 1.
Complete proteome.
SEQUENCE 431 AA; 44620 MW; 2DICA685248CCD3E CRC6
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-PAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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MEDLINE=21481971; PubMed=11598068;
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Matches 426; Conservative
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NUCLEOTIDE SEQUENCE
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NCBI_TaxID=1309;
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300

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K9_STRA3
QBE7X9_STRA3 PRELIMINARY;
QBE7X9;
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MEDINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
Iacobini B.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                  Length 447;
                                                                                                                                                                                                                                                                                                          58.1%; Score 1229.5; DB 2; Length
59.7%; Pred. No. 2e-48;
ive 42; Mismatches 99; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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46681 MW; F4DB14B0A5F962C8 CRC64;
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Last sequence update)
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                                 Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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InterPro; IPR009148; SibA.
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Q8E2H1;
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Matches 276; Conservative
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BEDLINE-2242508, PubMed-13354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Streptococcus agalactiae, a pathogen causing
emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002). EMBI; AEO14192; AAM98925.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                             Query Match

SB.1%; Score 1229.5; DB 2; Length 447;
Best Local Similarity 59.7%; Pred. No. 2e-48;
Matches 276; Conservative 42; Mismatches 99; Indels 45;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766843; CAD45661.1; -; Genomic_DNA.
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                                                                                      InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 447 AA; 46681 MW;
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                                                                                                                                                                    1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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Nat. Biotechnol. 22:1554-1558 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pubmed=15543133; DOI=10.1038/hbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
                                                                                                                DB 2; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311)
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                               58.1%; Score 1229.5; DB 2; Length
59.7%; Pred. No. 2e-48;
iive 42; Mismatches 99; Indels
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                                                                                        447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
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1-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (PCSB).
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=pcsB; OrderedLocusNames=stu0022;
        InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Féam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 447 AA; 46681 MW;
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Q5M6K4;
                                                                                                                                         Matches 276; Conservative
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NUCLEOTIDE SEQUENCE.
STRAIN=LMG 18311;
                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MGAS10394;
PubMed=15272401; DOI=10.1086/422697;
PubMed=15272401; DOI=10.1086/422697;
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
Voyich J.M., DeLeo F.K., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus
"Progress toward characterization of the macrolide-resistant serotype metagenome: complete genome sequence of a macrolide-resistant
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Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P., Decaris B., Leblond-Bourget N.;

"cse, a Chimeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";

J. Bacteriol. 187:2737-2746 (2005).

EMBL; CP0000023; AAV59752.1; -; Genomic_DNA.

EMBL; A730643; AAW82375.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 474;
                                                                                                                                                                                                                                                                                                                                                                            51.4%; Score 1087.5; DB 2; Length 51.7%; Pred. No. 6.18-42; ive 72; Mismatches 108; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                474 AA; 48142 MW; 1BAC6A9E0A0A200D CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                          PRINTS, PRO1852, SIBAPROTEIN.
PROSITE, PS50911, CHAP, 1.
Complete proteome.
SEQUENCE 474 AA, 48142 MW.
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Best Local Similarity
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NCBI_TaxID=301450;
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-; Genomic\_DNA.

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EMBL; AE009955; AAL96849.1;
          InterPro; IPR007921; CHAP. InterPro; IPR009148; SibA.
                                Pfam; PF05257; CHAP;
                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                             TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAABEBAARQAAAABA
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                                                                                                                                                        Gaps
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                                                                                                                                                        Indels 36;
                                                                                                                               Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                       42028 MW; 5DCEDA78CB863B60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative secreted protein.
OrderedLocusNames=spyMI8_0020;
                                                                                                                              51.4%; Score 1087; DB 2;
53.8%; Pred. No. 5.4e-42;
iive 56; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002)
       J. Infect. Dis. 190:727-738(2004).

EMBL; CP000003; AAT86152.1; -; Genomic_DNA.
InterPro; IPR001921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS0911; CHAP; 1.
Complete Protecome.
SEQUENCE 398 AA; 42028 MW; 5DCEDA78CB863Be
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WFNPTGVTFIYPH 398
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                                                                                                                                            Local Similarity 53.89
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Q7CNQ7;
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NUCLEOTIDE SEQUENCE
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MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Makagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
into phage evolution.";
Genome Res. 13:1042-1055(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                           51.4%; Score 1087; DB 2; Length 3 53.8%; Pred. No. 5.4e-42; ive 56; Mismatches 108; Indels
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Streptococcus pyogenes (serotype_M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                          SDCEDA78CB863B60 CRC64;
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                                                                                                                                                                          398 AA; 42028 MW;
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STRAIN=MGAS315 / Serotype M3;
PRINTS; PRO1852; SIBAPROTEIN. PROSITE; PS50911; CHAP; 1. Complete proteome. SEQUENCE 398 AA; 42028 MW;
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OrderedLocusNames=SPs0015,
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INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 OVSTLRTOKTELEAKNAELEKVSADLESEIQELSSKIVARODSLAKOARSAQONNTATSY
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                                                                                               "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
EMBL; CP000024; AAV61641.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D., Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D., Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J., Goffeau A., Hols P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   51.4%; Score 1087; DB 2; Length 485; ilarity 50.9%; Pred. No. 6.6e-42; Conservative 70; Mismatches 108; Indels 6
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                   485 AA; 49165 MW; 8665E4B1FC6CF7CA CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
10-MAY-2005 (TrEMBLrel. 30, Last ann
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PRINTS, PR01852, SIBAPROTEIN.
PROSITE, PS50911, CHAP; 1.
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Q9A1Z8; Q7BH59;
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tes 249; Conserv
                                                                                                                                                                                                                                                                                                                                                         Complete proteome
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  MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499; Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D. Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.; "Genome sequence of a service By Strain of group A Streptococcus; phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
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PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1087; DB 2; Length 3; Pred. No. 5.4e-42; 56; Mismatches 108; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
                                                                                                                                                                                            emergence.", prod. Sci. U.S.A. 99:10078-10083 (2002). EMBL, BAC0034; BAC63110.1; -; Genomic_DNA. EMBL, AE014136; AAM78621.1; -; Genomic_DNA. EMBL, AE014136; AAM78621.1; -; Genomic_DNA. InterPro; IPR007921; CHAP. InterPro; IPR009149; SibA. Pfam; PR02577; CHAP; 1. PRINTS; PR01852; SIBAPROTEIN. PROSTTE, PS0911; CHAP; 1. COMPLETE 7398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
Submit AE006474; AAK33158.1; -; Genomic_DNA.
EMBL; AF319999; AAL73135.1; -; Genomic_DNA.
EnterPro; IPR00921; GHAP.
FROMES; PRO1852; SIBAP.
COMPLETE PRO59911; CHAP; 1.
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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No.
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sequence 15, Appl Sequence 23, Appl Sequence 12307, A Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 11861, A Sequence 7646, Ap Sequence 7646, Ap Sequence 7647, Appl Sequence 12755, A Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	d Bush STREPTOCOCCUS PNEUMONIAE FOR DIAGNOS
US-08-302-756E-35 US-08-687-956A-23 US-08-489-03A-12307 US-08-06-676B-1 US-08-06-676B-1 US-08-28-414A-3 PCT-US-08-428-414A-3 PCT-US-09-949-016-7647 US-09-949-016-7647 US-09-949-016-7647 US-09-949-016-7647 US-09-489-033A-12755 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4 US-08-46-390-4	GNMENTS  3 3 3 4 4 10 AND AMING TO CS CS CS UTICS CORPOR UTICS CORPOR 60 60 60 60 60 60 60 60 60 60 60 60 60
10.0 9.8 9.7 9.7 9.5 9.5 9.5 9.5 9.5 9.5 9.5 9.5	SULT 1  SGUCHT 1  Sequence 3230, Application US/09107433  Patent No. 6800744  GENERAL INFORMATION:  GENERAL INFORMATION:  APPLICANT: Lynn A Doucette-Stamm a TITLE OF INVENTION: NUCLEIC ACID AND SEQUENCES: \$206  CORRESPONDENCE ADDRESS:  ADDRESSEE: GENOME THERAPEUTICS ADDRESSEE: GENOME THERAPEUTICS STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts COUNTRY: USA ZIP: 02354  COMPUTER: MASSACHUSETTS  COMPUTER: CUPKNOW: OPERATING SYSTEM: CUPKNOW: OPERATING SYSTEM: CUPKNOW: OPERATING SYSTEM: CUPKNOW: OPERATING SYSTEM: CUPKNOW: OPERATING SYSTEM: CUPKNOW: APPLICATION NUMBER: GO/051553  RILING DATE: 30-Un-1998  REDICATION NUMBER: GO/051553  ATTORNEY/AGRY INFORMATION: DAME: APPLICATION NUMBER: GO/051553  REPERENCE/DOCKET NUMBER: GC/051553  REPERENCE/DOCKET NUMBER: GC/051553  TELEPHONE: (791) 893-5007  TELEPHONE: (791) 893-5007  TELEPHONE: (791) 893-5007  TELEPHONE: (791) 893-5007  TELEPHONE: (791) 893-5007  TELEPHONE: TYPE: amino acids TYPE: amino acid TYPE: ami
28 206.51 30 206.53 31 201.5 32 201.5 34 201.5 36 195.3 37 195.3 39 194.5 41 193.5 44 193.5 45 193.5	RESULT 1 US-09-107-433-3230 Sequence 3230, A Patent No. 80007 Patent No. 80007 ITLE OF CORRESPON ADDR STRE CITY STAT COUN ADDR SOFT COUN ELLI PRIOR APPL PILI APPL PIL

us-10-797-821-32.rai

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61 QVSAIQAEQSNLQAENDRLQAESKKLEGEITELSKNIVSRNQSLEKQARSAQTNGAVTSY 120
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                                                            181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA
                                                                                                                                                                                                                               241 KRASQQQSV-----LASANTNLTAQVQAVSESAAAPVRAKVRPT-----LASANTNLTAQVQAVSESAAAPVRAKVRPT-----
                                                                                                                                                                                                                                                                       301 SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                                                                                                                                                                                                  361 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suri, Bruno
APPLICANT: Schmitz, Albert
ITILE OF INVENTION: Bacterial Vectors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATE: US 07/672,205
FILING DATE: 19-WAR-1991
APPLICATION UNMBER: GB 9006400.7
FILING DATE: 22-WAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/186,222 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-186-222-2; Sequence 2, Application US/08186222; Patent No. 5559007; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-TELECOMMINICATION:
TELEPHONE: (914)785-7121
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||
375 WFNPTTTSEGFVTYIY 390
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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COUNTRY: USA
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CITY: He
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TITLE OF INVENTION: Nacleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nacleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHON -0.74
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
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                                                                                                                                        8 MKKKILASLLLSTVMVSQVAVLTTAHAETTDDKIAAQDNKISNLTAQQQEAQKQVDQIQE
                                                                                                                                                                                               QVSALQTOQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
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                                                                                                                  1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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                                                                                Gaps
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                                                                                52;
                                      49.8%; Score 1053; DB 2; Length 399;
49.8%; Pred. No. 2.3e-73;
ive 74; Mismatches 93; Indels 5
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49.7%; Score 1052; DB 2; Length 392;
Best Local Similarity 49.8%; Pred. No. 2.6e-73;
Matches 217; Conservative 73; Mismatches 94; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4374, Application US/09583110
Patent No. 6699703
PARERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-583-110-4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 WFNP-----GSVSYIY 430
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382 WFNPTTTSEGFVTYIY 397
                                                                              Matches 217; Conservative
                                                          Similarity
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US-09-583-110-4374
    US-09-107-433-3230
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                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÓVSEINTÓAQDLLAKQDTLRQESAQLVKDIADLQERIEKREDTIQKQAREAQVSNTSSNY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 NTQAAQTGDSTDQSAAQAVNNSDQESTTA-----TAAQPSASSASTAAVAANTSS 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 ESTTPAPTTPSTDQSVDTGNGT-GSSTPAPTPTPTPEQPKPVTPAPAPSGSVNGAAIVAE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 AYKYIGTPYVWGGKDPSGFDCSGFTRYVYMQVTGRDIGGWTVPQESAGTKISVSQAKAGD 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VKKSLISAVMVCSMTLTAVASPIAAAADDFDSQIQQQDQKIADLKNQQADAQSQIDALES
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                             Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Youngman, Philip
APPLICANT: Fritz, Chrisian
APPLICANT: Fritz, Christopher
APPLICANT: Guzman, Luz-Maria
APPLICANT: Guzman, Luz-Maria
FILLE OP INVENTION: ESSENTAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 07334/060001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLFWGSQGGTYHVAIALG--GGO-YIHAPOPGESVKVGSVO-WFAP
                                                                                                                                                                                                                                                                                                                                                                                           Query Match

27.5%; Score 581.5; DB 2;
Best Local Similarity 30.4%; Pred. No. 8.1e-37;
Matches 160; Conservative 90; Mismatches 165;
                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...525
; SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
US-09-107-532A-5095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/222,938A CURRENT FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/09222938A Patent No. 6437108 GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION
                    TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
                                                               INFORMATION FOR SEQ ID NO: 5095:
                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                      14;
                                                                                                                                                  QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                             INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                    KAAAEBKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTDQ----SAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                             334 PAGQCT---WG-----VKSLAPWVGNYWGNGGQWAASAAAAG--YRVGSTPSAGAVA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSFSADFVGYANSPYGHVAIVKSVNSDGTITIKEGGY-GTTWWGHER-TVSASGVTFLMP 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AVĠĠĊŗĎYVWQYFAAQGIYIRNIMP-----ĠŇĠĠQWASNGPAQĠVLHVVĠAAP--ĠVIA 402
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                                                               1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                         TIAONTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA
                      Gaps
                      69;
                      Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
Best Local Similarity 35.6%; Pred. No. 1.9e-44;
Matches 171; Conservative 104; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATINIBLIO. Samela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5095, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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COMPUTER READABLE FORM
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US-09-107-532A-5095
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GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                ----NPGGSG 472
                                  ESTTTÓETTTSSTETESVVÍTPVÁÁAPEKEKEVPVTNPTTPEKGNEAKPGNGGVTSGKQÁ 366
                                                                                               375 SAGAVAVWNDG-----GYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWFNPGSVS 427
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 ----SASSASTA 321
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                                                                                                                                                                   427 QPGDVVQYESAYSPDSWIGGVHTVLVTGVSGGSVQIVEAN---
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
 DOSAAQAVNNSDQES----TTATAAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/071,035
                                                                                                                                                                                                                                                                                                                                               Sequence 482, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 482:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STATE: Maryland
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US-09-071-035-482
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Best Local
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1999-08-15
PRIOR FILING DATE: 1999-08-15
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                                                                                                                            Query Match 26.2%; Score 555; DB 2; Length 210; Best Local Similarity 54.8%; Pred. No. 2.7e-35; Matches 115; Conservative 44; Mismatches 51; Indels
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KLADDAQALTTKQAELKAAELSLAAEKATS 210
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FastSEQ for Windows Version 3.0
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US-09-134-000C-5990
IS-09-usence 5990, Application US/09134000C
; Patent No. 6617156
                                                                       ), ORGANISM: Streptococcus pneumoniae US-09-222-938A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Enterococcus faecalis
US-09-134-000C-5990
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 31.3%
Matches 152; Conservative
SOFTWARE: Fat
SEQ ID NO 67
LENGTH: 210
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Sequence 5714, Application US/09134000C
Sequence 5714, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: LYAIN DOUGETE-Stamm et al
APPLICANT: LYAIN DOUGETE-STAMM et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 80/055,778
SPRIOR APPLICATION NUMBER: US 80/055,778
                                                                                                                                                                                                                                                            QVSALQTQQAELQAENQRLEAQSATLGQQTQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                                                                                                                                                                  121 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQCTWGVKSLAPWVGNYWGNGGQWAASAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTG 395
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                                                                                    1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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        Gaps
    51;
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        87; Mismatches 177; Indels
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        138; Conservative
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TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
: : | : : | : : | ELETKRODILISKOSELNVMKASLALEQSSAESSKAGLEKOKAAAEAEQARLAAEQKAAAE 240
                                                                                                                                                                                                                                                                                                         AARQAAAAQAAAEAKAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAA----AADNT 281
                                                                                                                                                                                                                                                                                                                                                         241 KAKQAAAKPAKAKUK--AEAPVASSSTTEAQAPASSS--ATESSTQQTTETTTPSTDNS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAAQTGDSTDQSAAQAV-----NNSDQESTTATAAQPSASSASTAAVAANTSSANTYPA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQCTWGVKSLAPWVGNYWGNGGQWAASAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 G-----LRPVV---WDAGLAASATARAAQVEAGGIPNDH----WSRG--DEVIAIMW 399
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Pred. No. 3.4e-30;
                                                                                                                                     TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 VQGGQIQV---QEANYAGNQSIGNYRGW-FNPG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Dell Latitude
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTHARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILLING DATE: 29-Uni-2002
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369PlD1
INFORMATION FOR SEQ ID NO: 482:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 1998-05-04
PAPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
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APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INPORMATION:
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MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 482:
US-10-206-576-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
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Sequence 482, Application US/10206576

Patent No. 6913907

GENERAL INFORMATION:
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STRANDEDNESS: single
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30.5%;
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COMPUTER READABLE FORM:
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Best Local Similarity
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61 QEITNLNQRIEKRNEAIKNQARDVQVNGQSTTMLDAVLDADSVADAISRVQAVSTIVSAN 120
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Maryland
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Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                            282 QAAQTGDSTDQSAAQAV-----NNSDQESTTATAAQPSASSASTAAVAANTSSANTYPA 335
                                                                                                                                                            298 ATENTGSSSSEQPVÕPTTPSDNGNNGGÕTGGGTVTPTPEPTPAPSADPTINALNVLRQSL 357
                                                                                                                                                                                               336 GOCTWGVKSLAPWVGNYWGNGGOWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTG 395
                                                                                                                                                                                                                                358 G-----LRPVV---WDAGLAASATARAAQVEAGGIPNDH----WSRG--DEVIAIMW 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSAN 147
   ::|::| ::|::| ELETKRODLISKQSEINVWKASLALEQSSAESSKAGIEKQKAAAEAEQARLAAEQKAAAE 241
                                                        AARQAAAAQAAAEAKAAAEAKALQEQAAQAQAAAANNNNTQATDASDQQAA-----AADNT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGOVSALQTQQAELQAENQRLEAQSATLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Score 445.5; DB 2;
29.8%; Pred. No. 1.9e-26;
iive 80; Mismatches 168;
                                                                                                                                                                                                                                                                                          396 VQGGQIQV---QEANYAGNQSIGNYRGW-FNPG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: A Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
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amino acid
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Best Local Similarity 29.84
Matches 127; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-071-035-484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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Sequence 484, Application US/10206576

Patent No. 6913907

GENERAL INFORMATION:

APPLICATT: Choi et al.

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
148 EKMIHQQEQDKAAVEQKHQENQAAINTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL 207
                                                                                                                        208 TTAQDQKATLVAQKAAAE------EAARQAAAAQAAAEAKAAAEAKALQEQA 253
                                                                                                                                                                  254 AQAQAAANNNNTQATDASDQQAA----AADNTQAAQTGDSTDQSAAQAV-----NNSD 302
                                                                                                                                                                                                                                                                                           303 QESTTATAAQPSASSASTAAVAANTSSANTYPAGOCTWGVKSLAPWVGNYWGNGGQWAAS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                    297 QTGGGTVTPTPEPTPAPSADPTINALNVLROSLG------LRPVV----WDAGLAASAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 ARAAQVEAGGIPNDH----WSRG--DEVIAIMWAPGNSVIMAWYNETNMVTASGSG-HRD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 AAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQV---QEANYAGNQSIGNYRG
                                                       121 NDLMOQOKEDKOAVVDKKAENEKKVKQLEATEAELETKRODLLSKOSELNVMKASLALEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Dell Latitude
COMPUTER: Dell Latitude
COMPARE: SSYTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-011-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 60/041,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-10
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REGISTRATION NUMBER: 46,789
REPREBNCE/DOCKET NUMBER: PB369PID1
INFORMATION FOR SEQ ID NO: 484:
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 484:
US-10-206-576-484
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254

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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/054,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5035
                                                                                                                                                                                                   367 AAAAGSGNTKNSASGADINNYAGQIKSAIESKFYDASSYAGKTCTLRIK-LAPDGLLLNI 425
                                      251 AAAAKKAQQEAEKKAQQEAAKQAAAEKAAAEKAAEKAAAQKAAAE-KAAAEKAAAAEKAA 309
                                                                                    255 QAQAAANNNYTQATDASDQQAAAADNTQAAQTGDSTD------QSAAQAVNNSDQES 305
                                                                                                                             310 AAEKAAAD---KAAKAAAAKAAAAKKAAAAKEADGVDNLLGDLSSGKNAPKTGGGAKGNN 366
                                                                                                                                                                      306 TIAIAAQPSASSASIA-----AVAANISSANIYPAGQCTWGVKSLAP--WVGNY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 SNYNNYQ------SNNTQSQRTTQPTGGLGASYSTSSSNVHVTTTSA-PSSNGVS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480U2
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3244
LENGTH: 257
  AA---QLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEAKAAAEAKALQEQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 ANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQAVNNSDQESTTATAAQPSASSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 0 TAAVAANTSSANTYPAGOCTWGV-KSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Gaps
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                                                                                                                                                                                                                                                               353 WGNGGQWA-ASAAAGYRVGSTPSAGAVAVW 382
                                                                                                                                                                                                                                                                                                        426 QSEGGDPALCQAALAAARQAKFPKPPSQAVY 456
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Patent No. 6703492
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US-09-710-279-3244
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Best Local S
Matches 60
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE PEFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 0000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PELING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
                                                                                                                                                                      148 EKMLHQQEQDKAAVEQKHQENQAAINTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL 207
                                                                                                                                                                                                                                                                                          ----EAARQAAAAQAAAEAKAAAEAKALQEQA 253
                                                                                                                                                                                                                                                                                                                                                                              SAESSKAGLEKQKAAAEAEQARLAAEQKAAAEKAKQAAAKPAKAEVK--AEAPVASSST 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWAAS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTGGGTVTPTPEPTPAPSADPTINALNVLRQSLG-----LRPVV---WDAGLAASAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 AAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQV---QEANYAGNQSIGNYRG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 ARAAQVEAGGIPNDH----WSRG--DEVIAIMWAPGNSVIMAWYNETNMVTASGSG-HRD 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 LOAGEAAKEAKEQ-------OKOAEEAAKAAAAKAKADAQAKEAGEAAAKAA 190
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                                                                                    DDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQAELQAENQRLEAQSATLG
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                                           51;
    Length 422;
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  ; Score 445.5; DB 2;
; Pred. No. 1.9e-26;
80; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13565, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                   TTAQDQKATLVAQKAAAB-----
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tch 21.1%;
al Similarity 29.8%;
127; Conservative 8
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us-10-797-821-32.rai

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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENDATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC-607

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-10-8

PRIOR FILING DATE: 1997-10-8

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                                                                                                                                                                                                                                                                                                Query Match 11.2%; Score 236; DB 2; Length 257; Best Local Similarity 34.9%; Pred. No. 1.5e-10; Matches 60; Conservative 26; Mismatches 70; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AVWNDGGYGHVAYVTGV-QGQIQVQEANYAGNQSIGNYRGWFNPGSVSYIY 430
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                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: synthetic; COTHER INFORMATION: amino acid sequence
US-09-710-279-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 236; DB 2; Length 267;
ilarity 34.9%; Pred. No. 1.6e-10;
Conservative 26; Mismatches 70; Indels 16;
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 60; Conserv
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55748, A 50255, Ap 2248, Ap 6539, Ap 6539, Ap 610, App 5110, App 120, App 120, App 1120, App 1120, App 114, App 113, App 114, App 69, App

21, A Appl Appl Appl

69, A 59321 65, A 89, A

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

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Title: Perfect score:

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                US-10-732-923-3295
US-10-282-122A-50526
US-10-732-923-2248
US-10-724-972A-6539
US-10-724-972A-5110
US-10-724-972A-5110
US-10-724-972A-5110
US-10-724-974-86
US-10-823-120
US-09-974-923-120
US-09-974-923-120
US-09-974-923-120
US-09-91-953-120
US-09-91-953-120
US-09-91-91-91-91
US-10-282-122A-59321
US-10-470-048B-65
US-10-470-048B-65
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100.0%; Pred. No. 1.9e-121;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TILE OF INVENTION: Immunogenicity of Glucan Bin
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR FILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PALENTH Version 3.2
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/10383930 Publication No. US20040127400A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 432; Conservative
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Sequence 31, Appl
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5197, Ap
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3056, Ap
3054, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA Main:*
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; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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US-10-797-821-33

US-10-474-792-600

US-10-472-928-4652

US-10-282-122A-57658

US-10-124-251-67

US-10-1035-484

US-10-206-576-482

US-10-206-576-484

US-10-206-576-484

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Sequence 31, Application US/10797821
; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
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                                                                                                                                                                                                 APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

ITILE OF INVENTION: Taubman, Martin A

ITILE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 2566-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT PILING DATE: 2003-03-03-03

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Version 3.2

LENGTH: 432
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                                                                                                                                        ; Sequence 31, Application US/10383930; Publication No. US20040127400A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus mutans US-10-383-930-31
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APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REPERRENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR PILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-08-08

PRIOR PILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 45
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                                           ASAAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW 420
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                                                                                                                                                                                                                                                 ; Sequence 32, Application US/10797821
; Publication No. US20050031633A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-32
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Best Local Similarity 100.
Matches 432; Conservative
                                                                                                        FNPGSVSYIYPN
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
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PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 30
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Sequence 30, Application US/10383930
Sequence 30, Application US/10383930
Publication No. US20040127400A1
SENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03,
PRIOR PILING DATE: 2002-08-08
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Pred. No. 2.1e-120;
1; Mismatches 2;
                      US/10/797,821
CURRENT APPLICATION NUMBER: US/10/797,8
CURRENT PILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 10/383,930
PRIOR PILING DATE: 2003-03-07
PRIOR PILING DATE: 2003-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 09/290,049
PRIOR APPLICATION NUMBER: 09/290,049
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
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; ORGANISM: Streptococcus mutans
US-10-797-821-31
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Matches 429; Conservative
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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens;
FILE REFERENCE: 25669-020
CURRENT FILING DATE: 2004-03-09;
PRIOR PELING DATE: 2003-03-09
PRIOR PELING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR PELING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
PRIOR PELING DATE: 2002-03-07
PRIOR PELING DATE: 1999-04-12
PRIOR PELING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-01-08
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                                                                                                      DB 4; Length 431;
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                                                                                                  Score 2074.5; DB 4;
Pred. No. 6.6e-119;
1; Mismatches 3;
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; ORGANISM: Streptococcus mutans US-10-383-930-30
                                                                                                  Query Match
Best Local Similarity 98.8%;
Matches 427; Conservative
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98.6%; Pred. No. 1.2e-118;
live 1; Mismatches 4;
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; Publication No. US20050031633A1
; GENERAL INFORMATION:

// ORGANISM: Streptococcus mutans
US-10-797-821-29
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APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REPERENCE: 25669-018
FILE REPERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
PRIOR PLICATION NUMBER: 60/402,483
PRIOR FILING DATE: 2002-08-08
PRIOR PLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2070.5; DB 4; Length 431;
Pred. No. 1.2e-118;
1; Mismatches 4; Indels 1;
                                                          Length
                                                                                       3; Indels
                                                           DB 5;
                                                          Score 2074.5; DB 5;
Pred. No. 6.6e-119;
1; Mismatches 3;
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; Sequence 29, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
TYPE: PRT / ORGANISM: Streptococcus mutans US-10-797-821-30
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Best Local Similarity 98.6
Matches 426; Conservative
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Best Local Similarity
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GENERAL INCREMENTATION

GENERAL INCREMENTATION

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT FILING DATE: 2004-03-09

FRIOR PRILOR APPLICATION NUMBER: 10/383,930

PRIOR FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR FILING DATE: 1099-04-12

PRIOR FILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/115,142

PRIOR APPLICATION NUMBER: 60/115,142

PRIOR APPLICATION NUMBER: 60/115,142

PRIOR APPLICATION NUMBER: 60/115,142

PRIOR PILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SEQ ID NOS: 45

LENGTH: 431
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                                                                                                                                                                                                                               ; Sequence 33, Application US/10797821
; Publication No. US20050031633A1
; GENERAL INFORMATION:
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APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-08-08
PRIOR PLING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/10383930 Publication No. US20040127400A1 GENERAL INFORMATION:
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; ORGANISM: Streptococcus mutans
US-10-383-930-33
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Best Local Similarity 98.4%;
Matches 425; Conservative
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Publication No. US20050020813A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: P026926W0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                   APPLICANT: Caduraky, Stephen
APPLICANT: Zaquraky, Robert
APPLICANT: Zaquraky, Robert
APPLICANT: Nickbarg, Bliot
APPLICANT: Winter, Lourie
TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REPRENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                              51.1%; Score 1081; DB 5; Length 39:
53.6%; Pred. No. 3.2e-58;
trive 56; Mismatches 109; Indels
                                                                                                      Sequence 600, Application US/10474792; Publication No. US20040236072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WFNPGSVSYIYPN 432
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WFNPTGVTFIYPH 398
432
                Best_Local Similarity 53.6
Matches 232; Conservative
FNPGSVSYIYPN
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US-10-472-928-4652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 KAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAAQTGDSTDQSAAQANNN 300
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; Publication No. US20050136404A1
; GENERAL IMPORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 TSAAAAGFRIGSTPQVGAIACWNDGGYGHVAVVTAVESTTRIQVSESNYAGNRTIGNHRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEBAARQAAABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 SDQESTTATAAQPSASSAASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 KRASQQQSV-----LASANTNLTAQVQAVSESAAAPVRAKVRPT-----LASANTNLTAQVQAVSESAAAPVRAKVRPT
                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: secreted 45 kd protein (usp45)
OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15904062 (0.E+01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                   49.8%; Score 1053; DB 5; Length 392;
49.8%; Pred. No. 1.6e-56;
tive 74; Mismatches 93; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02354
TTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <Unknown>
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                                                                                                                                                                                     LENGTH: 392
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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COUNTRY: USA
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Matches 217; Conservative
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Sequence 57658, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 399;
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49.8%; Pred. No. 1.7e-56;
tive 74; Mismatches 93;
                                                                                       APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pneumoniae
                                            APPLICATION NUMBER: US/10/617,320 FILING DATE: 10-Jul-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
                                                                                                                                                                                                                                                                                                                                LENGTH: 399 amino acide
TYPE: amino acid
TOPOLOGY: linear
MOLECULB TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                  TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.8%
Matches 217; Conservative
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RESULT 14 US-10-282-122A-57658

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61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Robert
APPLICANT: Yaunamoro, Robert
APPLICANT: Yu. H.
APPLICANT: Ku, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE OF INVENTIONS: IGAILINGS 100 DEBENDIAL GENER IN PLICOUS GARRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR PLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR PLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-110-23

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/257,931

PRIOR PLICATION NUMBER: 60/267,636

PRIOR PLICATION NUMBER: 60/267,636

PRIOR PLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

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PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-10

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PRIOR PLING DATE: 2001-02-10

PRIOR PLING DATE: 2001-02-10

PRIOR PLING DATE: 2001-02-10

PRIOR PLING DATE: 2001-03-11

PRIOR PLING DATE: 2001-03-11

PRIOR PLING DATE: 2001-03-11
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---WVGN--YWGNG-----YWGNG------GOWAASAAAAGYRVG-STPSAGA 378
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                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/10154251
; Sequence 67, Application US/10154251
; Publication No. US20030092024A1
; GENERAL INFORMATION:
; APPLICANT: Youngman, Philip
; APPLICANT: Wurphy, Christian
; APPLICANT: Murphy, Christian
; APPLICANT: Murphy, Christian
; APPLICANT: Wurphy, Christian
; TITLE OF INVENTON: ESSENTIAL BACTERIAL GENES AND THEIR USE
; TITLE OF INVENTON: ESSENTIAL BACTERIAL
; FILE REFERENCE: 06286-060002
; CURRENT APPLICATION NUMBER: US/10/154,251
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; RUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 210
                                                                                                                                                                                                            379 VAVW-NDGGYGHVAYVTGVQGQIQVQEANYAGNOSIGNYRGWFNP 423
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                                                    330 ANTYPA-----GQCTWGVKSLAP----
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48, Appl 59, Appl 2964, Ap 252, Appl 56, Appl 3188, Ap 323, Appl 3988, Ap 1052, Appl 1060, Appl 1460, Appl 48, Appl 1460, Appl

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Sequence 210, Application US/11052554A
Publication No. US2005028866A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR PILICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
RNUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 210
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                        US-10-995-561-1015
US-10-821-24-1076
US-11-019-711-51
US-11-019-711-51
US-11-019-711-59
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US-11-019-711-59
US-11-019-711-59
US-11-069-814-58
US-11-059-814-58
US-11-059-814-58
US-11-052-554A-223
US-11-052-554A-223
US-11-052-554A-223
US-11-053-626-1105
US-11-059-814-60
US-11-069-814-8
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Best Local Similarity
Matches 426; Conserv
RESULT 1
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248, App
49, Appl
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Sequence 252, App
                                                                                                2006, 18:30:27; Search time 8.33977 Seconds (without alignments) 736.166 Million cell updates/sec
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Sequence 3
Sequence 4
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/cgn2 6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
/cgn2 6/ptodata/2/pubpaa/USOF NEW PUB.pep:*
/cgn2 6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
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/cgn2 6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
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US-11-052-554A-353

US-11-052-554A-3

US-11-052-554A-3

US-11-052-554A-3

US-11-052-554A-3

US-10-873-528-109

US-10-873-528-109

US-10-873-528-109

US-10-873-528-109

US-10-793-626-1682

US-10-793-626-1682

US-10-793-626-1182

US-11-052-554A-211

US-10-875-78-112

US-10-875-78-112

US-10-875-517-144

US-10-875-517-145

US-10-875-517-145

US-10-875-517-145

US-10-875-517-145

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Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KQFLEKAVFTVAA----TAATVVLGNKMADAD-TYTLQEGDSFFSVAQRYHMDAYELAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 211;
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44.2%; Pred. No. 3.7e-19;
iive 25; Mismatches 60;
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CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SEQ ID NO 358

LENGTH: 544
                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT PILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Streptococcus mutans UA159
US-11-052-554A-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 358, Application US/11052554A; Publication No. US20050288866A1; GENERAL INFORMATION:
                        Sequence 352, Application US/11052554A
Publication No. US20050288866A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus mutans UA159
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Best Local Similarity 44.2<sup>§</sup>
Matches 95; Conservative
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Matches 143; Conserve
      US-11-052-554A-352
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LENGTH: 211
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30653/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PATENTIN VERSION 3.3
                                                                   420
                                                                                                              419
SDQESTTATEAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 QVSSLQSEQDKLTARNTELEALSKRFEGEIKALTSQIVARNEKLKNQARSAYKNNETSGY 117
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                                                                                            360 ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGQIQVQGANYAGNQSIGNYRGW
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US-11-052-554A-252
                                                                                                                                                                                                                                                                                                          ; Sequence 252, Application US/11052554A; Publication No. US20050288866A1; GENERAL INFORMATION:
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Best Local Similarity 53.8%
Matches 233; Conservative
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WFNPTGVTFIYPH 398
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US-11-052-554A-252
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LENGTH: 398
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Sequence 79, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
                                                                                                                                                                                                                                APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
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                        204 LQTSQGAYGHVAYVEGVNSNGSIRVSEMNYGHGAGVVTSRTISASQAASYNY
380 AVWNDGGYGHVAYVTGV-OGGOIOVQEANYAGNQSIGNYRGWFNPGSVSYIY
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PRIOR FILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 971
                                                                                                                                                              Sequence 3, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
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tes 96; Conserv
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US-11-052-554A-79
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Best Local S:
Matches 96
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                                                                     62 VAIWSEENGÖDDLKWYHASNDGSNQLTVHFNAENHGSKVGSYIAHAYITYTDGNRVGVNL 121
                                                                                                                    GQQIQTLSSKIVARNESLKQ---QARSAQKSNAATSYINAIINSKSVSDAINRVSA---- 139
                                                                                                                                                              122 GKRKLSLS----APQLSLKQGGLQLFSKLKPSAADQLFSAVWSDENGQDDLHWYTADADG 177
                                                                                                                                                                                                               ----IREVVSANEKMLHQQEQD----KAAVE-QKHQENQAAINTVAAN 178
                                                                                                                                                                                                                                          178 NTLAGYANHKGYGTYHVHTYLKQNGKMIPISAQDIDIPKPKVKIQIDKINDTSYDVVVNN 237
                                                                                                                                                                                                                                                                                                             ---QETIAQNTNALNTQQAQLEAAQLNLQAE-- 206
                                                                                                                                                                                                                                                                                                                                        238 VPPYISSVAIPVWSEQNGQDDLKWYQATKVADGIFKTTVYLKTHRFELGNYQAHIYGDSQ 297
                                                                                                                                                                                                                                                                                                                                                                                                    -------LITTAQDQKATLVAQKAABEBAARQAAAQAAABAKAAAEAKAA
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: 901348008
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PRILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATCHIN Ver. 2.1
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Best Local Similarity 34.9%; Pred. No. 2e-07;
Matches 60; Conservative 26; Mismatches 70; Indels 16;
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OTHER INFORMATION: amino acid sequence
US-10-793-626-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNYRGWFNP----GSVSYIYPN 432
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| S20 YISNFRGWFDDTTSYLGRLTYIYPD 544
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Publication No. US20050255478A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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LENGTH: 257
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                                                                                                                                                                                                                                                                                                                                             NAATSYINAIINSKSVSDAINRVSAIREVVSANEKWLHQQEQDKAAVEQKHQENQAAINT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 VAANQETIAQNTNALNTQQAQLEAAQLNLQ---AELTTAQDQKATLVAQKAAAEEAA--R 229
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                                                                                                                                                                                       Length 394;
                                                                                                                                                                                  10.7%; Score 226.5; DB 7; Length : ilarity 27.5%; Pred. No. 1.1e-06; Conservative 61; Mismatches 178; Indels
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APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REPERENCE: PWC/P21129WO
CURRENT FILING DATE: 2004-06-23
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 109, Application US/10873528; Publication No. US20050276814A1; GENERAL INFORMATION:
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                                                                                                                                   , ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 -----NTQATDASDQQAAAD--NTQAQTGDSTDQSAAQAVNN---- 300
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                                            67 TQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIIN 126
                                                                                                                                        127 SKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQETIAQNT 186
                                                                                                                                                                                                                                                                                                                                                                                                                              241 KAAAEAKALQEQAAQAQAAANNN----NTQATDASDQQAAAADNTQAAQTGDSTDQSAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 QAVNNSDQESTTATA-AQPSAS-SASTAAVA-ANTS---SANTYPAGOCTWGVKSLAPWV 349
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7 SAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQ 66
                                                                                                                                                                                                                                                                                                                                                      187 NALNTQQAQLE---AAQLNLQAELTTAQDQKATLVAQKAAAEEAARQA---AAAQAAAEA
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APPLICANT: Biosynaxus Incorporated
APPLICANT: Biosynaxus Incorporated
APPLICANT: Boster, Simon
APPLICANT: Poster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REPERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
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; ORGANISM: Staphylococcus epidermidis
US-10-485-517-413
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Publication No. US20050256299A1
GENERAL INFORMATION:
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LENGTH: 270
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285 QTGDST---DQSAAQA 297
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US-10-857-780-23
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187 STYWSDAKYWASNAANDGYQVDNTPSVGAIMQSTPGPYGHVAYVERINGDGSILISEMNY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GHTTHADAAE--NNNQQQST-----YNYSTTEVSF-SNSGNLYTSGQCTWYVYDKT 67
                                                                                                                                                            Sequence 1682, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2004-03-04
PRIOR RAPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
SETOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1682
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: 05/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-111-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
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COTHER INFORMATION: Description of Artificial Sequence: synthetic
FOTHER INFORMATION: amino acid sequence
US-10-793-626-1682
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JOTHER INFORMATION: Description of Artificial Sequence: synthetic
SOTHER INFORMATION: amino acid sequence
US-10-793-626-2870
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ORGANISM: Artificial Sequence
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Best Local Similarity 39.73
Matches 50; Conservative
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                                      409 AGNOSIGNYR 418
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Best Local Similarity
Matches 50; Conserv
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US-10-793-626-2870
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LENGTH: 157
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US-1U-BS)-(18U-23)
Sequence 23, Application US/1085780
publication No. US20050272043A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: RANWERS, STEFAN MATTHEW ROBERTS
APPLICANT: RANWERS, STEFAN MATTHEW ROBERTS
APPLICANT: APPLICANT: RANGERN, RATTHEW ROBERTS
APPLICANT: APPLICANT: APPLICANT: REMELAND, RIKARD HENRY
APPLICANT: MATTHEW ROBERTS
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: BO490-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT APPLICATION NUMBER: US/23,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR RILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 2101
TANDER DATE: 2101
TANDER DATE: 2101
287 GDSTDQSAAQAVNNSDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGV-KSL 345
                                                                                                                                                               68 GGKIGSTWGNANSWATAAQAAGFTVNNTPEEGAIMQSSEGAFGHVAFVESVNNDGSITVS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 EEAARQAAAAQAAAEAKAAAEAKALQEQAAQAQAAANNNNTQATDASDQQAAAADNTQAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                        20 GHTTHADAAE--NNNQQQST-----YNYSTTEVSF-SNSGNLYTSGQCTWYVYDKT
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Staphylococcus aureus
                                                                           92; Conservative
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109; Conserv
                                                     Best_Local Similarity
Matches 92; Conserv
US-10-793-626-3154
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              Sequence 211, Application US/11052554A
| Sequence 211, Application US/11052554A
| Publication No. US20050288866A1
| Publication No. US20050288866A1
| Publication No. US20050288866A1
| TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
| TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
| TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
| FILE REPRENCE: 30853/40359A
| CURRENT FILING DATE: 2005-02-07
| PRIOR FILING DATE: 2004-07-20
| PRIOR APPLICATION NUMBER: US 60/589,227
| PRIOR FILING DATE: 2004-07-20
| PRIOR PILING DATE: 2004-07-20
| PRIOR FILING DATE: 2004-07-20
| PRIOR FILING DATE: 2004-07-30
| PRIOR FILING DATE: 2004-07-30
| PRIOR FILING DATE: 2004-07-30
| PRIOR FILING DATE: 2004-07-30
| PRIOR FILING DATE: 2004-07-30
| PRIOR FILING DATE: 2004-07-30
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| PRIOR FILING DATE: 2004-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 TNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEBAARQAAAAQAAAEBAKAAAE 245
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Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 06/164,258
PRIOR PLICHING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 44772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9%; Score 188.5; DB 7; Length 1562; Best Local Similarity 26.3%; Pred. No. 0.00089; Matches 87; Conservative 57; Mismatches 116; Indels 71;
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                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Streptococcus mutans UA159
US-11-052-554A-211
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ORGANISM: Artificial Sequence
PEATURE:
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LENGTH: 1095
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77 LKEQVQSATTLDGVQTVKNSSQTLNTAMKGLRDSIANEATIKAGQNYTDASPNNRNEYDS 136
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:::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|
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                                                                                                                                                                                                                                                                                                                175 VAA-----NQETIAQNTNA----LNTQQAQLEAAQLNLQ------AELTTA
                                                                                                                                                                                                                                   13 GVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQAEL
                                                                                                                       Gaps
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Length 1095;
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                                                                                                                 Indels
     8.7%; Score 184.5; DB 6; 22.5%; Pred. No. 0.001;
                                                                                                                 60; Mismatches 166;
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| Publication No. US20050256299A1
| GENERAL INPORMATION:
| APPLICANT: University of Sheffield
| APPLICANT: Biosynexus Incorporated
| APPLICANT: Soster, Simon
| APPLICANT: Soster, Simon
| APPLICANT: Mond, James
| TITLE OF INVENTION: Antigenic Polypeptides
| FILE REFERENCE: PloO629WO
| CURRENT APPLICATION NUMBER: US/10/485,517
| CURRENT FILING DATE: 2004-02-02
| PRIOR APPLICATION NUMBER: GB 0118825.9
| PRIOR APPLICATION NUMBER: GB 0200349.9
| PRIOR APPLICATION NUMBER: GB 0200349.9
| NUMBER OF SEQ ID NOS: 424
| SEQ ID NO 1444
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	Description	Add93653 Streptoco	Adx37276 Streptoco	Add93650 Streptoco	Adx37273 Streptoco	Add93649 Streptoco	Adx37272 Streptoco	Aeb91500 Microbial	Add93651 Streptoco	Adx37274 Streptoco	Add93652 Streptoco	Adx37275 Streptoco	Abp29684 Streptoco		Adv88392 Streptoco	Adv81808 Streptoco	Adv79645 Streptoco	Aeb91542 Microbial	Abp25919 Streptoco	Adr83884 S. pyogen	Abp25918 Streptoco	Abu02747 S. pneumo	Adt50226 S pneumon	Adt50165 S_pneumon	Adr94595 Novel S.
SUMMARIES	ID	ADD93653	ADX37276	ADD93650	ADX37273	ADD93649	ADX37272	AEB91500	ADD93651	ADX37274	ADD93652	ADX37275	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645	AEB91542	ABP25919	ADR83884	ABP25918	ABU02747	ADT50226	ADT50165	ADR94595
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## ALIGNMENTS

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B. ADD93653 standard; protein; 431 AA. 07-MAR-2002; 2002US-0363209P. 08-AUG-2002; 2002US-0402483P. 07-MAR-2003; 2003WO-US006962. (first entry) Taubman MA; Streptococcus mutans. (FORS-) FORSYTH INST. WPI; 2003-845091/78. GENBANK; AY046414. WO2003075845-A2. 29-JAN-2004 18-SEP-2003. Smith DJ, ADD93653; ADD9365 

Claim 5; Page 8-9; 49pp; English.

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 5SM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (MHC) caries. The compositions comprise major histocompatibilty complex (CHC) covalently linked with peptides upbunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiplicationspeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in

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New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries
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                                                                                                               The invention relates to a composition comprising a fragment of a gl binding protein-B (GbpB) and a biocompatible microparticle, where th fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds Streptococcus mutans GbpB protein of the invention.
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100.0%; Pred. No. 7e-134;
ive 0; Mismatches 0;
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                                                                                          Claim 3; SEQ ID NO 33; 73pp; English.
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microparticle; major histocompatibility complex; tooth disease.
                                              Length 431;
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-046280P.
08-AUG-2002; 2003US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                         Similarity
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                       Sequence 431
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Pred. No. 2.8e-133;
0; Mismatches 2;
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               07-MAR-2003; 2003WO-US006962
                                              07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
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Best Local Similarity 99.5%;
Matches 429; Conservative
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241 KAAAEAKALQEQAAQAQAAANNYTQATDASDQQAAAADNYQAAQTGDSTEQSAAQAVNNS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                       immunogenicity, immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                                                                           Streptococcus mutant glucan binding protein B variant #2
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                                                                                                                                                                                                                                                                                                                  99US-0115142P.
99US-00290049.
2002US-0363209P.
                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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(TAUB/) TAUBMAN M A.
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08-AUG-2002;
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12-APR-1999;
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WPI; 2003-845091/78.
GENBANK; AY046410.
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18-SEP-2003
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     SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF
DQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWAA
                      SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF
                                                                                                                         Streptococcus mutans glucan binding protein-B.
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/note= "HLA-binding peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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to a major histocompatibility complex
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Pred. No. 5.3e-133;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                           Composition useful as vaccines for a glucan binding protein-B binding class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 7; 49pp; English.
07-MAR-2003; 2003WO-US006962.
                                                   2002US-0363209P.
2002US-0402483P.
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Best Local Similarity 99.3
Matches 428; Conservative
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WO2005076010-A2.
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                                                                                                                                                                                         AEB91500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      binding protein-B (GbpB) and a blocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 KAAAEAKALQEQAAQAQVAANNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNS 300
                                                                                                                                                                                                                                                                                                                                                            New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                            immunogenicity, immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 431;
                                                                        Streptococcus mutant glucan binding protein B variant #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 29; 73pp; English.
           ADX37272 standard; protein; 431 AA
                                                                                                                                                                                                            13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-0029049.
07-MAR-2002; 2002US-03632099.
08-AUG-2002; 2002US-0402483P.
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                                                                                                                             Streptococcus mutans
                                                                                                                                                                                                                                                                                      (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
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                                                                                                                                               US2005031633-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 431 AA;
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                                                                                                                                                                                                                                                                                                                      Smith DJ,
                               ADX37272;
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life present interaction and adhearn-like proteins, by computing the sequence-
based attributes of protein sequences using five attribute modules of a
cerval network software, training an artificial neural network (ANN) for
each of the computed five attributes, and identifying the adheain and
adhesin-like proteins having probability of being an adhesin and
cequal or greater than 0.51. Also claimed is a set of 274 annotated genes
encoding adhesin and adhesin-like proteins, having 274 fully defined 162-
1151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical
genes encoding adhesin and adhesin-like proteins, having 105 fully
ceffined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated
adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base
pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-
Ike proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO:
280-384) sequences; and a fully connected multilayer feed forward ANN (I)
based on (MI). (MI) is useful for identifying adhesin and adhesin-like
proteins, of therapeutic potential, and identifying and short-liking
proteins for further testing in development of new vaccine formulations
to eliminate diseases caused by various pathogenic organisms. (MI) is
useful for identifying putative adhesins that are important in drug
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301 DOESTTATEAOPSASSASTAAVAANTSSANTYPAGOCTWGVKSLAPWVGNYWGNGGOWAA
                                                                                                                                         361 SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF
                                                                                        SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF
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20-JUL-2004; 2004US-0589227P.
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identifies adhesins from
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gastric ulcer and urinary tract infections. (M1) identifies adhesins fro distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
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                                                                                                     Length 431;
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                                                                                                    Score 2092; DB 9;
Pred. No. 5.3e-133;
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                                                                                                    99.4%;
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Matches 428; Conservative
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                                                     protein sequence
                                                                            Sequence 431 AA;
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                                                                                                                   The present sequence is the protein sequence of the glucan binding protein.B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions compositions and vaccines for dental (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against WHC class II binding fragments of GbpB can be used in passive immunisation.
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                       Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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                                                                                                                                                                                                                                                                                                                                                                        98.6%; Score 2075.5; DB 7; Length 432; 98.6%; Pred. No. 6.9e-132; ive 2; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutant glucan binding protein B variant #3.
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                                                                                             Claim 5; Page 8; 49pp; English.
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GENBANK; AY046412
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                                                                                                                                                                                                                                                                                                                                           Sequence 432
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419
                                                                                                                                                                                                                                                                                            The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                          New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 2075.5; DB 9 Pred. No. 6.9e-132;
                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 31; 73pp; English
                                                                             13-APR-1998; 98US-0081550P.
08-JAN.1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03632209P.
08-AUG-2002; 2003US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                        mammals against dental caries.
                                                          09-MAR-2004; 2004US-00797821
                                                                                                                                                                                                                                                                                                                                                                                        98.6%;
98.6%;
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                                                                                                                                                                                  Smith DJ, Taubman MA;
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 Streptococcus mutans
                                                                                                                                                   (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                      WPI; 2005-151644/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibity complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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                                                                                                                                                                                                              Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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Pred. No. 2.8e-131;
1; Mismatches 5;
                                                                                                                                                         Streptococcus mutans glucan binding protein-B.
ADD93652 standard; protein; 432 AA
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98.4%;
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2002US-0402483P.
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                                                                                                                                                                                                                                                                    Streptococcus mutans
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08-AUG-2002;
                                                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a fragment of a glucan binding protein-B (dpbB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
KAAAEBKALOGOAAQAAANNINITOATDASDQOAAADNIQAAQTGDSTDQSAAQAVINI
                                                                                    SDQESTTATAAQPSASSASTAAVAANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                         SDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                    ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTTGVQGGQIQVQEANYAGNQSIGNYRGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenicity, immune stimulation; glucan binding protein-B;
microparticle, major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutant glucan binding protein B variant
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Pred. No. 2.8e-131;
1; Mismatches 5;
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08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein;
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                                                                                                                                                                                                                                             FNPGSVSYIYPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIT/) SMITH D J. (TAUB/) TAUBMAN M A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
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12-APR-1999;
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1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
QVSALQTQQAELQAENQRLEAQSATLGQQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
                                                                                                                        121 INAIINSKSVSDAINRVSAIREVVSANEKMLHQQEQDKAAVEQKHQENQAAINTVAANQE
                                                                                                                                                                  INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE
                                                                                                                                                     TIAONTNALNTOOAQLEAAQLNLQAELTTAQDOKATLVAQKAAAEEAARQAAAAAA
                                                                                                                                                                                                        KAAAEAKALQEQAAQAQAAA-NNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNN
                                                                                                                                                                                                                                                              SDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWA
                                                                                                                                                                                                                                                                                                                   ASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGW
                                          OVSALOTOGAELQAENORLEAGSATLGQOIQTLSSKIVARNESLKQQARSAQKSNAATSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus polypeptide SEQ ID NO 8544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP29684 standard; protein; 447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                                                                                                                                                                                                         FNPGSVSYIYPN 431
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae.
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(GENO-) INST GENOMIC RES.
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Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antilnflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAABA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune stimulation, antigen; bacterial surface display; hyperimmune serum reactive antigen; vaccine; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                             chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                     Length 447;
                                                                                                                                                                                                                                                                                                                                                                                      94; Indels
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                                                                                                                                                                                                                                                                                                                                                   58.8%; Score 1238; DB 5; 60.7%; Pred. No. 2.7e-75;
                                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      Matches 280; Conservative
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                                                                                                                                                                                                                                                                                   Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                  Sequence 447 AA;
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vector comprising the nucleic acid molecule; a host cell comprising the vector; a hyperimmune serum-reactive antiquens of consisting of eig., 85, 299, 467 or 812 amino acids; fragments of hyperimmune serum-reactive antiquens consisting of peptides comprising e.g., 76, 134, 221 or 576 amino acids; consisting of peptides comprising e.g., 76, 134, 221 or 576 amino acids; consisting of peptides comprising e.g., 76, 134, 221 or 576 amino acids; captive antiquens erum-reactive antiquens a process for producing a cell that expresses a S. agalactiae hyperimmune serum reactive antiquen; a pharmaceutical composition, especially a vaccine, comprising the hyperimmune serum-reactive antiquen; a nucleic acid molecule; an antibody that binds at last to a selective part of the hyperimmune serum-reactive antiquen; a method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antiquen; a method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen; a method for identifying an expected or process for in vitro diagnosing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen to its interaction activity of a hyperimmune serum-reactive antigen to its interaction activity of a hyperimmune serum-reactive antigen to its interaction activity of a nucleic of a bacterial infection, especially a S. agalactiae infection. The hyperimmune serum reactive antigen is useful for solutional ribonucleic cacid molecule; hyperimmune serum reactive antigen, an interaction partner of a functional nucleic acid comprising apteners or spiegelmers. The nucleic acid comprising apteners or spiegelmers. The nucleic acid comprising apteners or spiegelmers. The nucleic acid comprising apteners or spiegelmers. The nucleic acid comprising apteners or spiegelmers or siRNA, The nucleic acid molecule, hyperimmune serum reactive antigen or antibody is untisense nucleic acid sequence of a Streptococcus agalactiae process for the mannifacture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment. Also described are: a vector comprising the nucleic acid molecule; a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding a hyperimmune serum reactive antigen, useful for the manufacture of a vaccine against Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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                                                                                                                                                                                                                                                       Prustomersky S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Gaps
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                                                                                                                                                                                                                                                       Horky M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; SEQ ID NO 219; 221pp; English.
                                                                                                                                                                                                                                                       Hanner M,
                                                                                       06-MAY-2004; 2004WO-EP004856.
                                                                                                                                     07-MAY-2003; 2003EP-00450112.
                                                                                                                                                             28-NOV-2003; 2003EP-00450266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 280; Conservative
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                                                                                                                                                                                                                                                                                                     WPI; 2004-821662/81.
                                                                                                                                                                                                                                                     Meinke A, Nagy E,
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                                                                                                                                                                                                                                                                                                                           N-PSDB; ADU69307
WO2004099242-A2.
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                                           18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel Streptococcus agalactiae nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II; ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S. agalactiae involved in the synthesis of amino acids, cell membranes, intermediate (central) metabolism, energetic metabolism, fatty acid and primidines and/or nucleotide metabolism including purines, pyrimidines and/or nucleotide metabolism including purines, pyrimidines and/or nucleotide metabolism including purines, conditions, sensitivity to medicines and/or analogues, functions related to transposens, biosynthesis of cofactors, prosthetic groups and to transposens, biosynthesis of cofactors, prosthetic groups and transporters, cell membrane proteins and cellular machinery. (I) are useful for the detection and/or amplification of nucleic acids. Pharmaceutical composition comprising (I) or (II) are useful for treatment of a bacterial S. agalactiae infection. Note: WO200292818AZ is
                           240
                                                    237
                                                                                KAAAEAKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTE--QSAAQAVN 298
                                                                                                           286
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                                                                                                                                                                                          CTWGVKSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVW--NDGGYGHVAYVTG 394
                                                                                                                                                                                                           CTWGAKSMASWVGNYWGNANOWGASARAAGYSVGTTPRVGAVAVWPYDGGGYGHVAVVTS 406
INTILNSKSVSDAVNRVVAIREVVSANEKMLAQQEADKAALEAKQIENQNAINTVAANKQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                          TI A QNTINALINT Q QAQLEAA QLINLQAEL TTA Q D QKATLVA QKAAA EEAAR QAAAAAA
                                                                                                                                      NSDQESTTATEA------OPS----ASSASTAVVTA------NTSSANTYPAGO
                                                                                                                                                             SATIVATITATATNEPKVIQPSVVIKAVEAPKAVVSSIPRAVSKPVVRSYDSSNIYPMGQ
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Poyart C, Trieu CP, Kunst
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                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus agalactiae protein sequence, SEQ ID 786
                                                                                                                                                                                                                                                                Antibacterial; Vaccine; bacterial infection.
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                                                                                                                                                                                                                                                                                                                                              ADV88392 standard; protein; 447 AA
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(CNRS ) CNRS CENT NAT RECH SCI.
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Couve E, B
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                                                                                                                              Gaps
equivalent for the present basic patent FR2824074A1. WO200292818A2 contains 6617 sequence whereas the present patent only contains 2344
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                                                                                                Length 447;
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Poyart C, Trieu-Cuot
                                                                                            58.8%; Score 1238; DB 8; Length 4 60.7%; Pred. No. 2.7e-75; ive 43; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 VANNSSIQVMESNYAGNMSIGNYRGSFNPSASGSVYYIYPN 447
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Couve E, Buchrieser C,
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nes 280; Conservative
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                                                                 Sequence 447 AA;
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Zouine M,
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QVSALQTQQABLQABNQRLBAQSATLGQQIQTLSSKIVARNBSLKQQARSAQKSNAATSY 1204
                                                                                                                                  The present invention relates to novel Streptococcus agalactiae

nucleotide sequences (1; ADV78860-ADV78998 and ADV83341-ADV85476) and

nucleotide sequences (1; ADV78860-ADV78998 and ADV83341-ADV85476) and

nucleotide sequences encode polypeptides of S. agalactiae involved in the

synthesis of amino acids, cell membranes, intermediate (central)

c synthesis of amino acids, cell membranes, intermediate (central)

c mclaotide metabolism including purines, pyrimidines and/or nucleosides,

regulatory functions, replication, transcription, translation, protein

transport, adaptation to atypical conditions, sensitivity to medicines

c and/or analogues, functions related to transpoons, biosynthesis of

cofactors, prosthetic groups and transporters, cell membrane proteins and

cellular machinery. (1) are useful for the detection and/or amplification

of nucleic acids. Pharmaceutical composition comprising (1) or (11) are

useful for treatment of a bacterial S. agalactiae infection. The complete

genome of Streptococcus agalactiae is given in ADV81204. Note: The

present patent is an equivalent for the basic patent FR2824074A1, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.8%; Score 1238; DB 8; Length 447;
60.7%; Pred. No. 2.7e-75;
iive 43; Mismatches 94; Indels 44; Gaps 10;
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Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
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                                                                                             Claim 6; SEQ ID NO 2949; 439pp; French.
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Best Local Similarity 60.73
Matches 280; Conservative
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Db 407 VANNSSIQVMESNYAGNMASIGNYRGSFNPSASGSVYYIYPN 447
Search completed: February 15, 2006, 18:03:01
Job time: 114.491 secs

V-OGGOIQVQEANYAGNOSIGNYRGWFNP---GSVSYIYPN 431

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238 299 287

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GenCore version 5.1.7
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OM protein - protein search, using sw model

February 15, 2006, 18:03:21; Search time 20.9676 Seconds (without alignments) 1977.789 Million cell updates/sec Run on:

US-10-797-821-33 2105 1 MKKRILSAVLVSGVTLSSAT.....SIGNYRGWFNPGSVSYIYPN 431 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.		Query Match	Length	DB	ΙD	Description
-	1057.5	50.2	392	2	G95258	secreted 45 kd pro
7	1057.5	50.2	392	~	B98124	stress
9	673	32.0	461	7	7600NC	ď
4	661.5	31.4	456	7	E86903	
S	551	26.2	507	~	805542	
Q	359.5	17.1	398	7	AC1763	peptidoglycan lyti
7	346	16.4	401	7	AI1387	doglycan
80	319.5	15.2	473	7	F70031	cell wall-binding
6	266	12.6	581	~	E75383	conserved hypothet
10	259	12.3	436	0	AH1387	wall
11	257.5	12.2	461	~	H84099	wall-
12	256.5	12.2	437	~	AB1763	cell wall binding
13	238.5	11.3	528	~	B75310	rved
14	230.5	11.0	421	2	JV0057	ein -
15	227	10.8	971	N	B90835	probable tail fibe
16	227	10.8	973	~	C85693	
17	226	10.7	394	~	F90725	membrane spanning
18	226	10.7	394	N	G85576	membrane spanning
19	225.5	10.7	166	7	C90029	hypothetical prote
20	223.5	10.6	267	~	F90028	
21	222.5	10.6	265	7	B89837	hetical
22	221.5	-	392	7	F96937	cell wall-associat
23	221.5	10	492	~	A28616	M5 protein precurs
24	220.5	10.5	4776	7	E95206	cell wall surface
25	220	10.5	255	~	G90061	14
26	217.5	10.3	1122	N	G64887	probable tail fibe
27	215	۲	688	~	317	conserved hypothet
28	214	10.	536	N	m	r17 transdu
29	212.5	10.1	483	7	A26297	M6 protein - Strep

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361 SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRGW 419

probable secreted	cell Burrace and	surface antigen A	FmtB protein [impo	M24 protein precur	IgA-specific metal	transcription acti	proteophosphoglyca	M protein precurso	hypothetical prote	IgA-specific metal	Htr8 transducer [i	IgA-specific metal	hypothetical prote	uncharacterized pr	M protein precurso
134852	/00/	460338	090011	428549	A81937	S66736	T30608	A60115	T13606	S61314	H84305	C81169	386865	B97273	S30284
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## ALIGNMENTS

RESULT 1 G95258	
 secreted 45 kd	45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Date: 03-Aug-	C;Decres: Streptococcus pheumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C, Accession: G: R, Tettelin, H.;	Jozso ; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heide
 on, J.D.; Umaya nson, T.; Hicke	on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 45	98-506, 2001 B. F. Wann B. Smith W.O. Wanton J.C. Danchartin B.A. Marrison
A; Title: Comple	A;Authors: Joillas, D. V., Authors, Johnson, M. W., Feller, O. C., Dougustry, D. M., Politzen, A. A. Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number:	nber: A95000; MUID:21357209; PMID:11463916
 A;Status: preliminary	25.25 minary
 A; Molecule type: DNA	e: DNA
A; Residues: 1-392 < KUR>	
A, Cross-referen	A, Cross-references: UNIPROT: Q97055; UNIPROT: Q8DMY4; UNIPARC: UP10000051B81; GB: AE005672; F
A; Experimental	Arkyperimental source: strain Tick4
A;Gene: SP2216	
Overv Match	50.2%; Score 1057.5; DB 2; Length 392;
Best Local Similarity	50.6%; Pred. No. 2e-44;
Matches 220;	220; Conservative 73; Mismatches 91; Indels 51; Gaps 5;
0y 1 M	MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG 60
Db 1 M	
 δλ (1)	VVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
 D 90	
 Qy 121 I	INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQCENQAAINTVAANQE 180
Db 121 I	-
Qy 181 T	ITAONTNALNTOOAQLEAAQLNLOAELTTAQDOKATLVAQKAAAEEAARQAAAAQAAAEA 240
181 K	
Qy 241 K	KAAAEAKALGEQAAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNS 300
Db 240 -	240EKRASQQQSVLASANTNLTAQ

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Similarity
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                                                                                                                Greetal stress protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Dacession: B90124
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E R; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M. Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Attle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 «KUR»
A;Residues: 1-392 «KUR»
A;Residues: 1-392 «KUR»
A;Gene: gsp-781
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C;Species: Lactococcus lactis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JN097
R;van Asseldonk, M.; Rutten, G.; Oteman, M.; Siezen, R.J.; de Vos, W.M.; Simons,
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                                                  FNPTTTSEGFVTYIY 390
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A;Title: Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis A;Reference number: JN0097; MUID:91071599; PMID:2123812
A;Accession: JN0097
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <VAN>
A;Residues: 1-461 <VAN>
A;Cross-references: UNIPARC:UP1000016D72B; GB:M35374
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çy Q	181 TIAONTNALNTOOAOLEAAOLNLOAELTTAODOKATLVAOKAAAEEAAROAAAAAA 240 ::	ò a	395 VQGGQIQVQEANYAGNQSIGNYRGWFNP 422 
& 8	241 KAAAEAKALGEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGBSTEQ-SAAQAVNN 299 	RESULT 6 AC1763 peptidog	RESULT 6 ACLTAC Debtidoalycan lytic protein P45 [imported] - Listeria innocua (strain Clip11262)
දු දු	300 SDQESTTATEAQPSASSASTAVVTANTSSANTYPAGO 336	C, Specie C, Date: C, Access	innocua #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
S da	337 CTWGVKSLAPWVGNYWGNCGQWAASAAAGYRVGSTPSAGAVAV 380	K;Glaser, 1; Domingue D.; Jones, Science 294	rone, F.; Bloeck n, K.D.; Faihi,
රු සි	381WNDGGYGHVAVYTGV-QGGQIQVQEANYAGNQSIGNYRGWFNPGSVSYIYPN 431 402 ADFVGYANSPYGHVAIVKSVNSNGTITIKEGGY-GTTWMGHER-TVSASGVTFLMPN 456	A; Author ok, C.; A; Title: A; Refere A; Access	Ajaunoss: Kretr, v. j. Kumi, m.; Kumi, m.; Kumier, r.; Kutapkat, G.; Madueno, E.; Mattouinem, A.; Matook, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vaqquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species. Ajreference number: AB1077; MUID:21537279; PMID:11679669
RESULT S S05542 hypothetic; Species C; Species C; Date: 0°	RESULT 5 805542 hypothetical protein, 54K - Enterococcus faecium C;Specias: Enterococcus faecium C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: S05542	A,Status: pr A,Molecule 1 A,Residues: A,Cross-ref A,Experiment C,Genetics: A,Gene: spl	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-398 «GLA A;Residues: 1-398 «GLA A;Residues: UNIPROT:Q92778; UNIPARC:UPI0000CC935; GB:AL592022; PIDN:CAC97875.1; A;Experimental source: strain Clip11262 C;Genetics: A;Gene: spl
R; Fuerst, Nucleic A A; Title: A A; Referent	P.; Moesch, H.U.; Solloz, M. koids Res. 17, 6724, 1989 A protein of unusual composition from Enterococcus faecium. ce number: S05542; MUID:89385998; PMID:2780297	Query Match Best Local a Matches 11:	/ Match Local Similarity 27.0%; Pred. No. 9.7e-11; les 113; Conservative 89; Mismatches 146; Indels 71; Gaps 16;
A; Accessi A; Molecul A; Residue A; Cross-re	.On: SUS542. e type: DNA ss: 1-507 <fue> references: UNIPROT:P13692; UNIPARC:UPI000016F6FC; GB:X16421; EMBL:M26048; NID:g</fue>	ò q	1 MKKRILSAV-LVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQAAQAQVNTIQ 59 
Query Match Best Local Matches 14	Query Match  Query Match  Best Local Similarity 28.9%; Pred. No. 7.3e-20;  Matches 147; Conservative 93; Mismatches 166; Indels 102; Gaps 13;	රු යි	GQVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATS :
& <del>Q</del>	10 LVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQ 69 ::  ::  :	රු පු ර	
& 8	70 AELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKS 129	os os	NTVAANGETIAQNTNAANTQOAQLEAAQLNLQAELTTAQDQXATLVAQXAAAEEAAKQAA :
රු දු	130 VSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQETIAQNTNAL 189 	è 8 6	
oy Q	190 NTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQ 235 	ờ a ሪ	
cy qa	236 AAAEAKAAAEEAKALOEQAAQAQAAANNNTQATDASDQQAAAADNTQ 281       :     :     : : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : : :   :	රු සි	345AFWGENYMGENGGOWAAAAAGTRVGSIFSAGAAWWW DGGIGTATATGVGGGGA 400 315 FRAAGVGLPRTSGGQYAAASKISASQAKPGDLVFFNYGGGIAHVGIYVGGGQM 367
ð a ð	282 AAQTGDSTEGSAAQAVNNSDQESTTATEAQPSASSASTAVVT 323 :       : :     : :       : :	RESULT 7 A11387 peptidog C;Specie C;Date:	RESULT 7 AI1387 peptidoglycan lytic protein P45 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

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A,Accession: E75383
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-581 <WHI>
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A,Map position: 1
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cell wall-binding protein homolog yvcE - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F70031
R;Munst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Chc
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A;Authors: Yoshkawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Yata, K.; Yoshida, R.;
A;Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUD:98044033; PMID:9384377
C;Accession: A11387

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Domiguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001

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A;Accession: A11387

A;Accession: A11387

A;Molecule type: DNA

A;Residues: 1-401 <GLA>

A;Residues: 1-401 <GLA>

A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YINAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQ-----QENQA-AI 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AAQAVNNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAG------QCTWGVKSL- 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 VASNDNNSAPSAAT-----PSSGGYSAMISAANAQLGKPYSLGATGPSAFDCS-GFTSYA 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         16.4%; Score 346; DB 2; 26.3%; Pred. No. 4.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110; Conservative
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C;Genetics:
A;Gene: spl
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A;Accession: F70031
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-473 <KUN>
A;Residues: 1-473 <KUN>
A;Cross-references: UNIPROT:P40767; UNIPARC:UPI000060AE1; GB:Z99121; GB:AL009126; NID:G;
A;Experimental source: strain 168
C;Genetics:
A;Gene:yvcE
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A;Experimental source: strain R1
C;Genetics:
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T.; Zalewski,
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75383
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Vencer, J.C.; Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 VE-----QKQQENQAAINTVAANQETIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 KATLVAOKAAAEEAAROAAAAQAAEAKAAAEAKALOEQAAQAQAAANNNTQATDASDQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 ASELANOKANTE-----SEQARIKKEQEAAALIKKÖEEAOKA-----SDETQTDDSÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 AISVGSSIVGOSP----YKFGGGRTQSDINNRIFDCSSFVRWAYASAGVNLGPVGGTTTD
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                                                                                                                                                                                                                                                                                         Length 473;
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                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                      15.2%; Score 319.5; DB 2; 24.0%; Pred. No. 9.9e-09; iive 95; Mismatches 186;
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Matches 111; Conservative
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Matches 122; Conservative
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R.J.; F C.; Ma}

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Db 127 QTTGTATSYLDMIFEADDFKELVDRVTVVSAIVKADQNIMQDQKDDQDKLKVAESTSEKK 186  Qy 170 AA-INTVAANQETIAQNTNALNTOQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAA 228  187 LENLKVLAVELEVSKNNMESOKQEKNDLVMALAN-KKDLTKSEQTLLASEQGALTDEE 243  Qy 229 RQAAAQAAEAKAAAEAKAAAEAKAAAAANNTQATDASDQQAAADNTQAAQTGDS 288  229 RQAAAQAAEAKAAAEAKAAAEAKAAAAAAAAASTAVVTANTSSANTYPAGGCTWGV 341  E	RESULT 11 H84099 ccl wall-binding protein BH3600 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: H84099 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hiran Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and § A;Accession: H84099 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-461 <stc> A;Accession: H8409 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-461 <stc> A;Cross-references: UNIPROT: Q9K6X4; UNIPARC: UPI00000C424C; GB:AP001519; GB:BA000004; NID A;Experimental source: strain C-125 C;Genetics: C;Genetics: A;Gene: BH3600</stc></stc>	Query Match         12.2%;         Score 257.5;         DB 2;         Length 461;           Best Local Similarity 22.1%;         Pred. No. 9.5e-06;         11;         12.3%         13.5         Mismatches 180;         11dels 91;         Gaps 11;           Qy         31 DAQIASQDSKINNLTAQQQAQQVNTIQGQVSALQTQQAELQAENQRELEAQSATLGQQI 90         11;         11;         11;         11;         11;           Db         56 EABLKEVEKELGDITABIERLDKEVEETSGKIQEKREEIEEVQAEIEELKEQI 108         91 QTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSANEKM 150         108         11;         11;         11;         11;         10         11;         11;         12;         12;         11;         10         10         EILBERRIABRDELLKORARAMYQNGGSIDYLEVILGAKSFGDFLDRVSALSVIA	Qy 151 Db 163 Qy 211 Db 211	Qy
	OY 274 AAADNTQAAQTGDSTEQSAAQAVNNSDQESTTATEAQPSAS 315	C.Accession: AH1387 R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker. r.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 Science 294, 849-852, 2001 A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species. A.Accession: AH1387 A;Accession: AH1387 A;Status: preliminary A;Accession: AH1387 A;Status: preliminary A;Molacule vipe: DNA	A;Cross_references: UNIPROT:08Y4E2; UNIPARC:UPI0000055221; GB:NC_003210; PIDN:CAD00582.1 A;Experimental Bource: strain EGD-e C;Genetics: A;Gene: lmo2504 Query Match 12.3%; Score 259; DB 2; Length 436; Best Local Similarity 22.8%; Pred. No. 7.5e-06; Matches 97; Conservative 90; Mismatches 152; Indels 86; Gaps 14;	Qy         6 LSAVLVSG-VTLSSATTLSAV

14;

Gaps

49;

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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mab S.; Smith, H.O.; Vanter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75310
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-528 «WHI>
A;Residues: 1-528 «WHI>
A;Resperimental source: strain R1
C;Genetics:
A;Genetics:
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C;Species: Escherichia coli
C;Species: D7-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produc A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Molecule type: DNA
A;Residues: 1-421 <-LEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AAQAAAEAKAAAEAKALQEQAAQAQAAAANNNTQATDASDQQAAAADNTQAAQTGDSTEQS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 QAQRRAE---QAQARAEQVQ-AQAQAAA------QASVRQAQQAAQTQLGQVRTGAAQQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 LQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESL----KQQARSAQKSNAATSY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 VLSGMAISAASLAAFILL------NRNAVSTIAQADQLRPQIEALRTEVGTVQGELRA 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 238.5; DB 2; 29.1%; Pred. No. 9e-05; ive 53; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AAQAVNNSDQESTTATEAQPSAS 315
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Best Local Similarity
Matches 94; Conserv
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Cell wall binding protein homolog lin2647 [imported] - Listeria innocua (strain Clip1126 Cell wall binding protein homolog lin2647 [imported] - Listeria innocua (strain Clip1126 C; Species: Listeria innocua
C; Species: Listeria innocua
C; Date: 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: AB1763
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
C; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AB1763
A; Status preliminary
A; Molecule type: DNA
A; Residues: 1-437 < GLA>
A; Cross-references: UNIPROT:0927Y9; UNIPARC:UPI00000CC934; GB:AL592022; PIDN:CAC97874.1;
A; Experimental source: strain Clip11262
C; Genetics:
A; Genetics:
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B75310
Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 09-Jul-2004
C;Accession: B75310
E;R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
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Pred. No. 1e-05;
                                                                   -QIQVQEANYAGNQSIGNYRGWFN 421
                                                                                                                   LHFEVHEGSYRGSSSAVNPMNYIN 461
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24.1%;
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222 ASTATTKASEAASSARDASASKEAAKSSETSAASSASSAASSATAAGNSAKAAKTSETNA 281
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                                                                                                                                                                                                                                                                                                                              342 GEATEQASAAASSASAAKTSETNAKASETSAESSKTAAASSASSASSASSASKDEAT 401
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139 AIREVVSANEKMLQQQEQDKAAVEQKQQENQAAIN-TVAANQETIAQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKQ-QARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QKQQENQAAI--NTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL-TTAQDQKATLV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AÇKKAEAAAAALKKKAEAAEAAAAEARKKAATEAAEKAKAEAEKKAAAEKAADKKA--A 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AOKAAAE-EAAROAAAAAAAAEAKAAAEAKALOEQAAQAAANNNT---QATDASDQQA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 AAADNTQAAQTGDSTEQSAAQAVNNSDQESTTATEAQ-PSASSASTAVVTANTSSANTYP 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 IISAVL--HVILFAALIWSS-----FDENIEASAGGGGGSIDAVMVDSGAVVEQYKRMQ
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                                                                                                                                                                                                                                                                   Length 421;
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                                                                                                                                                                                                                                                            11.0%; Score 230.5; DB 2; Length 28.2%; Pred. No. 0.00017; ive 67; Mismatches 177; Indels
                                                                                                       protein
                                                                                             C'Keywords: nucleotide binding; P-loop; transmembrane F:14-34/Domain: transmembrane #status predicted <MSS> F:14-34/Domain: helical #status predicted <HSR> P:355-362/Region: nucleotide-binding motif A (P-loop)
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Matches 116; Conservative
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                                      A;Map position:
A;Start codon: G
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121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
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Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; ANO46414; ARV94540-1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR007921; CHAP.

PETAN; PR05277; CHAP.

PRINTS; PR05277; CHAP.

PRINTS; PR0511; CHAP.

PROSITE; PS50911; CHAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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                100.0%; Score 2105; DB 2; Length 431; 100.0%; Pred. No. 2.9e-86; o; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=5SM3;
MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=5SM3;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
(Cloning of the gppB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44650 MW; 05D38D8D8BC4609F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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                                                    05M137_STRT1
08BXT4_STRA3
08BXT4_STRA3
09278_L15IN
071W53_L15MF
09RE04_L15MF
06M552_CORGL
08UAV2_BACCR
08UAV2_BACCR
073DG0_BACCI
                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                      STRMU
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Q8NQA0_CORG
Q73DG0_BACC
YVCE_BACSU
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Q8DUR7_8
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    Q938V0 STRMU PRELIMINARY;
Q938V0;
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Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
Tidentification of stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
                                                                        KAAAEAKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNS
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DOI=10.1128/IAI.69.11.6931-6941.2001,
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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MEDLINE=21153617; PubMed=11254612;
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Q9AG98;
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NUCLEOTIDE SEQUENCE.
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01-FEB-2005
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.P., Chen T., Smith D.J.,
Duncan M.J.;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                PRINTS; PRO1852; SIMAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44592 MW; 3EBE21FC5E47232E CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Infect. Immun. 69:6931-6941(2001).
EMBL; AF338445; AAK08104.1; -; Genomic_DNA.
EMBL; AY046411; AAK04501.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
PF05257; CHAP; 1.
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Q938V3;
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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0938V2.
0918C2-
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
61ucan-binding protein B.
5treptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
Cloning of the gppB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
                                                                                                                                                 2D1CA685248CCD3E CRC64;
                                                                                                                                                                                      99.4%; Score 2092; DB 2;
99.3%; Pred. No. 1.1e-85;
iive 0; Mismatches 3;
EMBL; AE014855; AANS7811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PP05257; CHAP; 1.
                                                                                                                                                 431 AA; 44620 MW;
                                                                                  PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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SEQUENCE 431 AA; 44620 MW;
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NCBI_TaxID=1309;
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  protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:631-6941(2001).
EMBL. AVO46410; AAX94500.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
Ferretti J.J.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
                                                                                                                                                                                                                                                                           3; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                                                                                                                                                                                               Score 2092; DB 2;
Pred. No. 1.1e-85;
0; Mismatches 3;
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                                                                                                                           Pfam, PF05257, CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44650 MW;
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Q8DWM3;
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"Identification and molecular analysis of PcsB, a protein required for cell wall separation of group B streptococcus.";
U. Bacteriol. 183:1175-1183(2001).
EMBL: AJ277292; CAC28144-1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
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      protein B and analysis of genetic diversity and protein production in
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Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.2%; Score 2066.5; DB 2; Lengtlest Local Similarity 98.4%; Pred. No. 1.5e-84; Matches 425; Conservative 1; Mismatches 5; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                              50911; CHAP; 1.
432 AA; 44652 MW; 3F88ECB9A1F3BE4F CRC64;
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Last annotation update)
                           Cinical isolates,;
Infect. Immun. 69:6931-6941(2001).
EMBL. AV046413; AAK94503.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfan, PF02577; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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O9AKA4;
01-JUN-2001 (TrEMBLrel. 17, Cx
01-JUN-2001 (TrEMBLrel. 17, La
01-MAR-2004 (TrEMBLrel. 26, La
PCSB protein precursor.
Name=pcsB;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                  PRINTS; PRO1852; SIGAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW; E769B2504AEE50E9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AY046412; AAK94502.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches 426; Conservative
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NCBI_TaxID=1309;
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61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
EMBL; AE014192; AAM98925.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                          Length 447;
                                                                                                                                                                                                                                                        58.8%; Score 1238; DB 2; Length 4 60.7%; Pred. No. 1.1e-47; ive 43; Mismatches 94; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                  447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-QGGQIQVQEANYAGNQSIGNYRGWFNP---GSVSYIYPN
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invasive neonatal disease.";
MNI microbiol. 45:1499-1513(2002).
EMBL; AL766843; CAD45661.1; -; Genomic_DNA.
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                  Proc. Natl. Acad. Sci. U.S.A. 9
EMBL, ABO14192; AAM98925.1; -;
TIGR: SAG0017; -.
InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
Pfan; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete Protecome.
SEQUENCE 447 AA; 46681 MW;
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.79
Matches 280; Conservative
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QBE7X9 STRA3 PRELIMINARY;
QBE7X9;
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NCBI_TaxID=216495;
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                                                                                                                                                                                             Length 447;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                              447 PcsB protein.
46681 MW; F4DB14B0ASF962C8 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                         58.8%; Score 1238; DB 2; 60.7%; Pred. No. 1.1e-47; iive 43; Mismatches 94;
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                    Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
  InterPro; IPR009148; SibA.
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447 AA;
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                                                                                                                                44;
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Nat. Biotechnol. 22:1554-1558 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
Streptococcus.
                                                                                                        Length 447;
                                                                                                                               94; Indels
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                                                                                447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                       58.8%; Score 1238; DB 2; 60.7%; Pred. No. 1.1e-47;
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                                                                                                                               43; Mismatches
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Name=pcsB; OrderedLocusNames=stu0022;
        InterPro; IPR007921; CHAP.
InterPro; IPR00148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAROTEIN.
PROSITE; PS50911; CHAP; 1.
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                                                                                                                               280; Conservative
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NUCLEOTIDE SEQUENCE.
STRAIN=LMG 18311;
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PubMed=15272401; DOI=10.1086/422697;
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus
metagenome: complete genome sequence of a macrolide-resistant serotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAA----AQA
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Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P., Decaris B., Leblond-Bourget N.;
"cse, a Chimeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";
D. Bacteriol. 187:2737-2746(2005).
EMBL; CP000023; AAVS9752.1; -; Genomic_DNA.
EMBL; AX730643; AAW82375_1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.0%; Score 1095; DB 2; Length 4 Best Local Similarity 51.6%; Pred. No. 2.7e-41; Matches 246; Conservative 67; Mismatches 114; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                  474 AA; 48142 MW; 1BAC6A9E0A0A200D CRC64;
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PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 474 AA; 48142 MW.
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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QSXELL1;
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STRAIN=MGAS315 / Serotype M3;
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                                                                     Complete proteome
SEQUENCE 398 AA
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MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
                                                                                                                                                       Gaps
                                                                                                                                                       35;
                                                                                                                                DB 2; Length 398;
                                                                                                                             ; Score 1092.5; DB 2; Length
; Pred. No. 3e-41;
57; Mismatches 108; Indels
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Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                       5DCEDA78CB863B60 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
M6 strain.";
J. Infect. Dis. 190:727-738(2004).
J. Infect. Dis. 190:727-738(2004).
EMBL: CPRO0003; AAT86552.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
PF05557; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PSS9911; CHAP; 1.
COMDICE Protecome.
SEQUENCE 398 AA; 42028 MW; 5DCEDA78CB863B6
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Matches 232; Conservative
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Q7CNQ7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.9%; Score 1092.5; DB 2; Length 53.7%; Pred. No. 3e-41; ive 57; Mismatches 108; Indels
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Straptococcus pyogenes (serotype_M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                SDCEDA78CB863B60 CRC64;
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QBP318; Q7CFL7;
QBP318; Q7CFL7;
QBP318; Q7CFL7;
QBP318; Q7CFL7;
QBP318; Q7CFL7;
QBP318; Q7CFL7;
QBP318; Q7CFL7;
QBP318; Q7CFL7;
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QBP318; Q7CFL7; Q7CFL7;
QBP318; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7; Q7CFL7;
EMBL; AE009955; AAL96849.1; -; Genomic DNA.
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he Res. 13:1042-1055(2003)
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                                                                                                                                                                                                               PRINTS; PR01852; SIBAPROTEIN PROSITE; PS50911; CHAP; 1.
                                              InterPro; IPR007921; CHAP. InterPro; IPR009148; SibA.
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Complete proteome.
SEQUENCE 485 AA;
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MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499; Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Rammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D. Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Shlievert P.M., Musser J.M.; "Genome sequence of a service By Strain of group A Streptococcus: "Genome sequence of a service M.S. Strain of group A Streptococcus phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 398;
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PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
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Last annotation update)
                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002) EMBL; BA000034; BAC63110.1; -; Genomic_DNA. BMBL; AE014186; AAW78621.1; -; Genomic_DNA. InterPro; IPR007921; CRIAP. InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1092.5; DB 2;
; Pred. No. 3e-41;
57; Mismatches 108;
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FNPTGVTFIYPH 398
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Q5M212;
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OVSALOTOQAELQAENORLEAQSATLGOOTOTLSSKIVARNESLKQQARSAOKSNAATSY 120
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                                                                                          "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
EMBL: CF000024; AAVG1641.1; -; Genomic_DNA.
InterPro; IPR00921; CHAP.
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D., Ponstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D., Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J., Goffeau A., Hols P.,
                                                                                                                                                                                                                                                                                                                                                                                                                          51.7%; Score 1087.5; DB 2; Length 485; 50.8%; Pred. No. 6e-41; Live 67; Mismatches 112; Indels 61;
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                                                                                                                                                                                                                                                                                                                                                                        485 AA; 49165 MW; 8665E4B1FC6CF7CA CRC64;
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STRAIN=SF370 / ATCC 700294 / Serotype
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OrderedLocusNames=SPy0019;
                                                                                                                                                                                                                                                                Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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Q9A128_Q7BH59;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.8
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398; Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.; Mite J., "Complete genome sequence of an MI strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                               Fagan P.K., Reinscheid D., Gottschalk B., Chhatwal G.S., "Identification and characterization of a novel secreted protein from
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 398;
                                                                                                                                                                                                                                                                                                                                                     51.6%; Score 1085.5; DB 2; Length 53.7%; Pred. No. 6.1e-41; ive 57; Mismatches 108; Indels
                                                                                                                                                             group A streptococcus.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006474; AAK731158.1; -; Genomic_DNA.
EMBL; AF319999; AAL73135.1; -; Genomic_DNA.
EnterPro; IPR001918; SibA.
PRINTS; PR001918; SIBAP; 1.
ENGITE; PS0911; CHAP; 1.
Complete proteome; Signal.
                                                                                                                                                                                                                                                                                                                        SEQUENCE 398 AA; 41899 MW; 28A9B3F7195E969B CRC64;
                                                                                                                                                                                                                                                                                                            Potential [ ]
                                                                                                                                                                                                                                                                                                                                                                                 Matches 232; Conservative
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NUCLEOTIDE SEQUENCE
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Search completed: February 15, 2006, 18:09:17 Job time : 124.476 secs

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11, Appl
11, Appl
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2870, Ap
5441, Ap
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5453, Ap
                                                                                                       February 15, 2006, 18:09:37; Search time 29.9537 Seconds (without alignments) 1189.611 Million cell updates/sec
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Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/f_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE COMB.pep:*
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US-08-110-4374

US-08-110-4374

US-08-110-4374

US-09-110-532A-5095

US-09-222-938A-67

US-09-121-938A-67

US-09-134-000C-5910

US-09-071-035-482

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US-09-071-035-484

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                                                                                                                                                                                                                                                                                                                   572060 seqs, 82675679 residues
 GenCore version (c) 1993 - 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                   Copyright
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No.
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FOR DIAGNOS
                           Sequence 13307, A Sequence 13861, A Sequence 23, Appl Sequence 24, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 5, Appl Sequence 6, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Se
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Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
US-09-902-540-14908
US-09-489-039A-12307
US-09-902-540-13861
US-08-894-017-23
                                                                                                                                                          5352450-2

US-08-466-390-4

US-08-470-950-4

US-08-195-487-4

US-08-195-487-4

US-09-452-294-1

US-09-256-662-32

PCT-US-09-902-540-1

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US-09-949-016-7647
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APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1997
APPLICATION NUMBER: 60/08153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: AINIGHIO, PARMER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-607
TELEPHONE: REGISTRATICS:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 3230:
SEGUENCE CHARACTERISTICS:
                                                                                                   US-08-894-01/-23
US-09-456-474-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
      ORIGINAL SOURCE
      0000000000000000000
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241 KAAAEAKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNS 300
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61 QVSAIQAEQSNLQAENDRLQAESKKLEGEITELSKNIVSRNQSLEKQARSAQTNGAVTSY 120
                                  INAIINSKSVSDAINRVSAIREVVSANEKMLOOOEODKAAVEOKOOENQAAINTVAANOE 180
                                                                                                            181 TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240
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                                                                                                                             361 SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                      240 ----EKRASÓQÓSVLÁSÁNTNLTAÓ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suri, Bruno
APPLICANT: Schmitz, Albert
TITLE OF INVENTION: Bacterial Vectors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,205
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: GB 9006400.7
FILING DATE: 22-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/186,222 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-186-222-2
; Sequence 2, Application US/08186222
; Patent No. 5559007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30,598
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REPERBUNCI-DOCKET NUMBER: 4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914)785-7121
                                                                                                                                                                                                                                                                                                                                                                                                            FNP-----GSVSYIY 429
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Villamizar, JoAnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 461 amino acids
amino acid
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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US-08-186-222-2
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APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION:
Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
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                                                                                                                                                                                                                                                           121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 SAAAAAGFRTGSTPQVGAIACWNDGGYGHVAVVTAVESTTRIQVSESNYAGNRTIGNHRGW 382
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                                                                                                                                                                                     QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
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                                                                                                                               1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                                                                                                                                                                                                                                                                                                                                                                                            241 KAAAEAKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNS
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                                                                         Gaps
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                                                                         51;
                                    DB 2; Length 399;
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                                                                         91; Indels
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                                                      Pred. No. 9.4e-70
                                                                       73; Mismatches
                                  50.2%; Score 1057.5; 50.6%; Pred. No. 9.4e
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; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4374
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                                                                       Matches 220; Conservative
                                                      Local Similarity
JS-09-107-433-3230
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US-09-583-110-4374
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226 241

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121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.2%; Score 594; DB 2; Length 525; Best Local Similarity 31.0%; Pred. No. 1.3e-35; Matches 162; Conservative 92; Mismatches 163; Indels 106;
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; Patent No. 6437108
; GENERAL INFORMATION:
; APPLICANT: Youngman, Philip
; APPLICANT: Wurphy, Christian
; APPLICANT: Murphy, Christopher
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
; TILE REFERENCE: 07334/06001
; CURRENT APPLICANTON NUMBER: US/09/222,938A
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FASELSQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TIAONTNALNTOQAQLEAAOLNLOAELTTAODOKATLVAOKA----
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                                                                                                                                                                                                                                               ;
NAME/KEY: misc_feature
;
LOCATION: (B) LGCATION 1...525
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
US-09-107-532A-5095
                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                             LENGTH: 525 amino acids TYPE: amino acid
   SEQUENCE CHARACTERISTICS:
                                                                                   TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-222-938A-67
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LENGTH: 210
TYPE: PRT
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                 13;
                                                                                                                                                                                                                     61 QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY 120
                                                                                                                                                                                                                                                         121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
                                                                                                                                                                                                                                                                                                                                                                                        TIAQNTNALNTQQAQLEAAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAAEA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KAAAEAKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDSTEQ----SAAQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 Q------QKEAAQAQAASTAATAXAVEAATSSASASSQAPQVSTSTDNTTSNASASN 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AGQCT----WG------VKSLAPWVGNYWGNGGQWAASAAAAG--YRVGSTPSAGAVAV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 VGGCTDYVWQYFAAQGIYIRNIMP-----GNGGQWASNGPAQGVLHVVGAAP--GVIAS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 -----WNDGGYGHVAYVTGVQG-GQIQVQEANYAGNQSIGNYRGWFNPGSVSYIYPN 431
                                                                                                                                 1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
                                    Gaps
                                 68;
Best Local Similarity 35.2%; Pred. No. 2.5e-41;
Matches 169; Conservative 103; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 AVNNSDQESTTATEAQPSASSASTAVVTANTSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
COMPATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REFERENCE/DOCKET NUMBER: 40,489
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5095, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5095:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
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US-09-107-532A-5095
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Enterococcus faecalis Polynucleotides and Polypeptides
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321 VVTANTSSANTYPA-----GQCTWGVKSLAPWVGNYWGNGGQWAASAAAAGYRVG-STPS 374
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                                                                                375 AGAVAVWNDG-----GYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWFNPGSVSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: PP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
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                                                                                                                                                                                                                                                                                                                      Sequence 482, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: A. Anders Brookes
REGIESTRATION UNDRER: 36,373
REFRENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 482:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome SciensTREET: 9410 Key West Avenue
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amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
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Best Local Similarity 31.61
Matches 142; Conservative
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APPLICANT: Gil H. Choi
TITLE OF INVENTION: Ent
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APPLICATION NUMBER:
FILING DATE:
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CLASSIFICATION:
                                                                                                                                                                          428 IYPN 431
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Sequence 5990, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: UUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: UNTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT PRILION DATE: 1998-08-13

PRIOR PILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                   QVSALQTQQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSY
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                                                                                                              Gaps
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                                                                 DB 2; Length 210;
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                                                                 ; Score 562; DB 2;
; Pred. No. 9e-34;
45; Mismatches
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181 KLADDAQALTTKQAELKAAELSLAAEKATS 210
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    ORGANISM: Streptococcus pneumoniae
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US-09-134-000C-5990
                                                                 26.7%;
                                                                                     Best Local Similarity 55.29
Matches 116; Conservative
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        ; ORGANISM: Str
US-09-222-938A-67
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                                                                   Query Match
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DEFICEANT: LYON DOUGETEE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 5714
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                                                                                                                                                                                                                                                                                                                                                      TGDSTEQSAAQAV-----NNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCT 338
                                                                                                                                                                                                                                                                                                                                                                                             301 TGSSSSEQPVQPTTPSDNGNNGGQTGGGTVTPTPEPTPAPSADPTINALNVLRQSLG--- 357
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  1 VKKRLFASVLLCSLTLSAIATPSIALADNVDKKIEEKNQEISSLKAKQGDLASQVSSLEA
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                                         QVSALQTQQAELQAENQRLEAQSATLGQQTQTLSSKIVARNESLKQQARSAQKSNAATSY
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31.6%; Pred. No. 2.6e-29;
ive 88; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIQV---QEANYAGNQSIGNYRGW-FNPG 423
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ORGANISM: Enterococcus faecalis
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Matches 142; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 482, Application US/10206576
Patent No. 6913907
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 497
285 TGDSTEQSAAQAV-----NNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCT 338
                                                                                                                                                                             TGSSSSEQPVQPTTPSDNGNNGGQTGGGTVTPTPEPTPAPSADPTINALNVLRQSLG--- 357
                                                                                                                                                                                                                    339 WGVKSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGG 398
                                                                                                                                                                                                                                                         358 ----LRPVV----WDAGLAASATARAAQVEAGGIPNDH----WSRG--DEVIAIMWAPGN 403
                                                             -AKAAAEAKALQEQAAQAQAAANNNTQ-----ATDASDQQAA----AADNTQAAQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUMRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-UNI-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 482:
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 482:
                                                                                                                                                                                                                                                                                                   399 QIQV---QEANYAGNQSIGNYRGW-FNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JTER READABLE FORM:
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Best Local Similarity
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US-10-206-576-482
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Sequence 484, Application US/10206576

Patent No. 6913907

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                              241 AQAPASSSSATESSTQQTTETTTPSTDNSATENTGSSSSEQPVQPTTPSDNGNNGGQTGG 300
                                                                                                                                                                                                                                                                                                                                        350 QVEAGGIPNDH----WSRG--DEVIAIMWAPGNSVIMAMYNETNMVTASGSG-HRDWEIN 402
                                              208 TTAQDQKATLVAQKAAAE-EAARQAAAQAAAE-AKAAAEAKALQEQAAQAQAANNNTQ 265
                                                                                                                                   -----ATDASDQQAA----AADNTQAAQTGDSTEQSAAQAV-----NNSDQEST 305
                                                                                                                                                                                                                                                                 301 GTVTPTPEPTPAPSADPTINALNVLRQSLG-----LRPVV----WDAGLAASATARAA 349
                                                                                                                                                                                                                                                                                                             421
  121 NDLMQQQKEDKQAVVDKKAENEKKVKQLEATEAELETKRQDLLSKQSELNVMKASLALEQ 180
                                                                       306 TATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWAASAAAA
                                                                                                                                                                                                                                                                                                             366 GYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQV---QEANYAGNQSIGNYRGW-FN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/071,035
FILING DATE: 1990-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hyman, Mark J. '
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369PID1
INFORMATION FOR SEQ ID NO: 484:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 422 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                    PG 423
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SEQUENCE
US-10-206-576-484
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Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                          339 WGVKSLAPWVGNYWGNGGQWAASAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKMLQQQEQDKAAVEQKQQENQAAINTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL 207
TGDSTEQSAAQAV-----NNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCT 338
                                                                                                                                                                                                   ----LRPVV---WDAGLAASATARAAQVEAGGIPNDH----WSRG--DEVIAIMWAPGN 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSAN 147
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                                                                                                28 DDFDAQIASQDSKINNLTAQQQAAQAQVNTIOGQVSALQTQQAELQAENQRLEAQSATLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 2; Length 422;
9.4e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81; Mismatches 166;
                                                                                                                                                                                                                                                                          SVIMAWYNETNWVTASGSG-HRDWEINPG 432
                                                                                                                                                                                                                                                 399 QIQV---QEANYAGNQSIGNYRGW-FNPG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.8%; Score 458; 31.0%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/071,035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 484:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 31.0
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
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                                                                     285
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APPLICANT: LYON DOUGETE-Stamm et al APPLICANT: LYON DOUGETE-Stamm et al APPLICANT: LYON DOUGETE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: 1059-134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING PRIOR FILING DATE: 1997-11-08 PRIOR FILIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 NNYSNYNNYNNYQ---SNNTQSQRTTQPTGGLGASYSTSSSNVHVTTTSA-PSSNGVSLS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 VVTANTSSANTYPAGQCTWGV-KSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVA 379
                                                                310 AAEKAAAD--KAAKAAAAKAAAAKKAAAAKEADGVDNLLGDLSSGKNAPKTGGGAKGNNA 367
                                                                                                                                        294 AQAVNNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAP--WVGNY 351
                                                                                                                                                                                                             368 AAAGSGNTKNSASGADINNYAGQIKSA-IESKFYDASSYAGKTCTLRIK-LAPDGLLLNI 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 --NARSASGNLYTSGQCTYYVFDRVGGKIGSTWGNANNWANAAARSGYTVNNSPAKGAIL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT PEPLICATION NUMBER: U5/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PLILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CRGANISM: Artificial Sequence CRGANISM: Artificial Sequence FEATURE: FORTH INFORMATION: Description of Artificial Sequence: synthetic US-09-710-279-3244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 235; DB 2; 34.5%; Pred. No. 1.1e-09; tive 29; Mismatches 75
OAOAAANNNTOATDASDOOAAAADNTOAAQTGDSTE-
                                                                                                                                                                                                                                                                                         352 WGNGGQWA-ASAAAAGYRVGSTPSAGAVAVW 381
                                                                                                                                                                                                                                                                                                                                              426 QSEĞDPALCQAALAAARQAKFPKPPSQAVY 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3244, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
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Best Local Similarity
Matches 59; Conserva
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US-09-134-001C-5035
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US-09-710-279-3244
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APPLICANT: Gary Breton et. al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709 2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQ ID NOS: 14342
SEQ ID NO 13565
                                                                                                                                            147
                                                                                                                                                                                      148 EKMLQQQEQDKAAVEQKQENQAAINTVAANQETIAQNTNALNTQQAQLEAAQLNLQAEL 207
                                                                                                                                                                                                                                                                                                                                   TTAQDOKATLVAQKAAAE-EAARQAAAAQAAAE-AKAAAEAKALQEQAAQAQAANNNTQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 -----ATDASDQQAA----AADNTQAAQTGDSTEQSAAQAV-----NNSDQEST 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AQAPASSSSATESSTQQTTETTTPSTDNSATENTGSSSSEQPVQPTTPSDNGNNGGQTGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 TATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNGGQWAASAAAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEAQSATLGQQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 LOAOEAAKEAKEO-------OKOAEEAAAKAAAAKAKADAOAKEAOEAAAKAA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 GYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQV---QEANYAGNQSIGNYRGW-FN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 QVEAGGIPNDH----WSRG--DEVIAIMWAPGNSVIMAWYNETNMVTASGSG-HRDWEIN 402
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   87
                                         DDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQAELQAENQRLEAQSATLG
                                                                                                                                            QQIQTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKSVSDAINRVSAIREVVSAN
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28.4%; Pred. No. 1.7e-12;
tive 57; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13565, Application US/09489039A Patent No. 6610836
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.2%
Best Local Similarity 28.4%
Matches 111; Conservative
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US-09-489-039A-13565
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Sequence 4539, Application US/09134001C

Bacent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DELIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: E998-08-13
TITLE OF INVENTION UNMER: US 60/064,964
FRICK FILING DATE: 1997-11-08
FRICK FILING DATE: 1997-11-08
FRICK FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4539
LENGTH: 267
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                                                                                                                                                                  261 NNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNSDQESTTATEAQPSASSASTA 320
                                                                                                                                                                                                98 NNYNNYSNYNNYQ---SNNTQSQRTTQPTGGLGASYSTSSSNVHVTTTSA-PSSNGVSLS 153
                                                                                                                                                                                                                                                              321 VVTANTSSANTYPAGQCTWGV-KSLAPWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVA 379
                                                                                                                                                                                                                                                                                     261 NNNTQATDASDQQAAAADNTQAAQTGDSTEQSAAQAVNNSDQESTTATEAQPSASSASTA 320
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                                                                                                                                                                                                                                                                                                                                                                                      212 QTSQGAYGHVAYVEGVNSNGSIRVSEMNYGHGAGVUTSRTISASQAASYNY 262
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                                                                                                                     .;
8
                                                                Query Match
11.2%; Score 235; DB 2; Length 264;
Best Local Similarity 34.5%; Pred. No. 1.2e-09;
Matches 59; Conservative 29; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.2%; Score 235; DB 2; Length 267; Best Local Similarity 34.5%; Pred. No. 1.2e-09; Matches 59; Conservative 29; Mismatches 75; Indels
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5035
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US-09-134-001C-4539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QVSALQTQQAELQAENQRLEAQSATLGQQ1QTLSSKIVARNESLKQQARSAQKSNAATSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT PILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 41
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100.0%; Pred. No. 2e-120;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/10383930 Publication No. US20040127400A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-33
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Best Local Similarity 100.
Matches 431; Conservative
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/cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*
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Biocceleration Ltd.
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Listing first 45 summaries
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Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
US-10-282-122A-55748	US-10-282-122A-50526	US-10-732-923-3295	US-10-650-274-86	US-10-470-048B-362	US-10-724-972A-6539	US-10-724-972A-5110	US-09-971-536-69	US-10-282-122A-56483	US-09-874-923-120	US-09-991-496-120	US-09-820-843A-114	US-10-732-923-2248	US-10-470-048B-73	US-09-769-787-109	US-09-820-843A-113	US-10-470-048B-74	US-10-470-048B-89
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## ALIGNMENTS

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US-10-797-821-30
Sequence 30, Application US/10797821
Publication No. US20050031633A1
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
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JEDICANT: Smith, Daniel J

APPLICANT: Smith, Daniel J

APPLICANT: Smith, Daniel J

APPLICANT: Tandman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 5002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

SEQ ID NO 30

LENGTH: 431
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Pred. No. 7.1e-120;
0; Mismatches 2;
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; Publication No. US20040127400A1
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; ORGANISM: Streptococcus mutans
US-10-383-930-30
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Best Local Similarity 99.5%;
Matches 429; Conservative
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421 NPGSVSYIYPN 431
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GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT PILING DATE: 2004-03-09
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR PLILING DATE: 2002-03-07
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SEQ ID NOS: 45
SEQ ID NOS: 45
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                                              361 SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF 420
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                                                                                                                                                                                                                                                                            Sequence 33, Application US/10797821 Publication No. US20050031633A1
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; ORGANISM: Streptococcus mutans
US-10-797-821-33
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PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 29
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US-10-797-821-29
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US-10-383-930-29
; Sequence 29, Application US/10383930
; Sequence 29, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Sath, Daniel J
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
; FRIOR FILING DATE: 2002-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 431;
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               CURRENT FILING DATE: 2004-03-09
CURRENT FILING DATE: 2004-03-09
PRIOR PILING DATE: 2004-03-09
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 45
SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Streptococcus mutans
US-10-797-821-30
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     FILE REFERENCE: 25669-020
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APPLICANT: Taubman, Martin A.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: U5/383,930

PRIOR APPLICATION NUMBER: 06/363,209

PRIOR PILING DATE: 2003-03-07

PRIOR FILING DATE: 2003-03-07

PRIOR FILING DATE: 2002-03-07

PRIOR PILING DATE: 2002-03-07

PRIOR PILING DATE: 1999-04-12

PRIOR PILING DATE: 1999-04-12

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 29
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                                                                                                                                                                    Gaps
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                                                                                                                   Length 431;
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                                                                                                             Query Match 99.4%; Score 2092; DB 4; Best Local Similarity 99.3%; Pred. No. 1.3e-119; Matches 428; Conservative 0; Mismatches 3;
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-29
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### GENERAL INFVARATION:
| APPLICANT: Smith, Daniel J.
| APPLICANT: Smith, Daniel J.
| APPLICANT: Taubman, Martin A.
| TILE GVE INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REFERENCE: 25669-020
| CURRENT APPLICATION NUMBER: US/10/797,821
| CURRENT FILING DATE: 2004-03-09
| PRIOR PILING DATE: 2002-03-07
| PRIOR PILING DATE: 2002-03-07
| PRIOR FILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 1999-04-13
| PRIOR PILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-01-08
| NUMBER OF SEQ ID NOS: 45
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 31
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; Publication No. US20050031633A1
; GENERAL INFORMATION:
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APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 2569-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT PILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR PLING DATE: 2002-08-08
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 41
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                                                                                                Length 431;
                                                                                                                                    Indels
                                                                                              Score 2092; DB 5;
Pred. No. 1.3e-119;
                                                                                                                                  0; Mismatches
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; Sequence 31, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
                   TYPE: PRT ; ORGANISM: Streptococcus mutans US-10-797-821-29
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US-10-383-930-31
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Best Local Similarity 98.6
Matches 426; Conservative
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NPGSVSYIYPN 431
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 LENGTH: 431
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Sequence 32, Application US/10797821

Publication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 2569-020

CURRENT FILING DATE: 2004-03-09

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR PILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-01-08

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 32

LENGTH: 432

LENGTH: 432
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Matches 425; Conserv
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APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REPERBORS: 2566-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT APPLICATION NUMBER: 00/402,483
PRIOR PILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PALENTIN version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 432;
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Pred. No. 4.5e-118;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-383-930-32
; Sequence 32, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Streptococcus mutans US-10-383-930-32
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Best Local Similarity 98.4%;
Matches 425; Conservative
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RESULT 13
US-10-617-320-3230
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Ublication No. US20050020813A1

GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026926W0
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                    APPLICANT: Olmeted, Stephen
APPLICANT: Zagursky, Robert
APPLICANT: Nickbary, Elliot
APPLICANT: Nickbary, Elliot
APPLICANT: Nickbary, Lourie
TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
SEQ ID NO 600
                                                                                                                                                                                                                                                                                                                                                                                  51.6%; Score 1085.5; DB 5; Length
53.7%; Pred. No. 2.6e-58;
tive 57; Mismatches 108; Indels
                                                                                              Sequence 600, Application US/10474792
Publication No. US20040236072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-600
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FNPTGVTFIYPH 398
                       FNPGSVSYIYPN 432
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Best Local Similarity
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US-10-472-928-4652
                                                                                    US-10-474-792-600
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Publication No. US20050136404A1
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette STAMM AMINO ACID
TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THEAPPLASHOUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKRILSAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQG
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                     OTHER INFORMATION: secreted 45 kd protein (usp45)
OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15904062 (0.E+01)
                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
50.2%; Score 1057.5; DB 5; Length 392;
Best Local Similarity 50.6%; Pred. No. 1.3e-56;
Matches 220; Conservative 73; Mismatches 91; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EKRÁSÓQÓSVLÁSANTNLTAQ-----
CURRENT APPLICATION NUMBER: US/10/472,928
                CURRENT FILING DATE: 2003-09-26
PRIOR PAPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SEQ ID NO 4652
LENGTH: 392
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <Unknown>
                                                                                                                                                                                 TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5206
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COUNTRY: USA
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034 A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-26
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2001-02-09
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PRIOR PELING DATE: 2001
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31.2%; Pred. No. 1.9e-28;
tive 91; Mismatches 163; Indels 106;
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Sequence 57658, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Enterococcus faecium
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Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.2%; Score 1057.5; DB 50.6%; Pred. No. 1.3e-56 tive 73; Mismatches 9
                                                                       PRICATION DATE: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/095131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Actinical Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPROME: (781)893-5007
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LOCATION: (B) LOCATION 1...399

SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
9S-10-617-320-3230
  OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 399 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
                                                           CURRENT APPLICATION DATA:
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FNPTTTSEGFVTYIY 397
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity 50.69
Matches 220; Conservative
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282 AAQTGDSTEQSAAQAVNNSDQESTTATEA------QPSASSASTAVVTANTSSANT 331

RESULT 14 US-10-282-122A-57658

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301 ESTTPESSTEESTAPESSATEESTTVPESSATEESTTVPESSTTEEST 360
                                                                                                                                                                       361 TPAPTTPSTDQSVDTGNGT-GSSTPAPTPTPTPEQPKPVTPAPAPSGSVNGAAIVAEAYK 419
                                                                                                                                                                                                                                                347 WVGN--YWGNG-----YWGNG------GOWAASAAAGYRVG-STPSAGAVAV 380
                                                                                                                                                                                                                                                                                               121 INAIINSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQE 180
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Sequence 67, Application US/10154251

Publication No. US20030092024A1

SEGNERAL INFORMATION:
APPLICANT: Voungman, Philip
APPLICANT: Murphy, Christian
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maxia
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 2002-09-16
FILE REFERENCE: 2002-09-16
FRIOR PAPLICATION NUMBER: US/10/154,251
CURRENT FILING DATE: 2002-09-16
FRIOR PELLING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 210

TYPE: PRICE
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                                                                                                                                                                                                                                                                                                                                                                                                                               W-NDGGYGHVAYVTGVQGGOIQVQEANYAGNQSIGNYRGWFNP 422
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                                                                                                         332 YPA-----GQCTWGVKSLAP
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Best Local Simi
Matches 116;
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Matches 428; Conservative
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Publication No. US2005028866A1

GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.

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TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
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                                                                                                                                                   US-10-467-657-270

US-10-485-517-252

US-11-019-711-59

US-10-793-626-2098

US-10-793-626-1098

US-10-793-626-1052

US-10-793-626-1052

US-10-793-626-1016

US-11-019-711-49

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; ORGANISM: Streptococcus mutans UA159
US-11-052-554A-210
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Sequence 352, Application US/11052554A
Publication No. US2005028866A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
FILE REPERRNCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT PILING DATE: 2005-02-07

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: 2004-02-06

LENGTH: 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 APWVGNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGV-QGGQIQVQ 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 211;
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus mutans UA159
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US-11-052-554A-358
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Matches 143; Conservative
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                                                                                                                                                                                                                                                                                          Sequence 252, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-00
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361 SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF 420
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                                                               SAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQGGQIQVQEANYAGNQSIGNYRGWF
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US-11-052-554A-252
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SOFWARE: Patentin version 3.3
SEQ ID NO 252
LENCTH: 398
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APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIREVVSANEKMLQQQEQDKAAVEQKQQENQAAIN-TVAANQETIAQN-----TNA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASTATTKASEAASSARDASASKEAAKSSETSAASSASSAASSATAAGNSAKAAKTSETNA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQSAAQAVNNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 ASTTKKGIVQLSSATNSTSESLAATPKAVKAAYELANGKYTAQDATTAQKGIVQLSNATN 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNTQQAQLE-----AAQLNLQAELTTAQDQKATLVAQKAAAEEAARQAAA---- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 KSSETAAEQSASAAAGSKTAAALSASAASTSAGQASASATAAGKSAESAASSASTATTKA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----QAAAEAKAAAEAKALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTGDST 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 ATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAVNTIQGQVSALQTQQAELQAENQR
                       380 VWNDGGYGHVAYVTGV-QGGQIQVQEANYAGNQSIGNYRGWFNPGSVSYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%; Score 227; DB 7; L 23.8%; Pred. No. 4.5e-06; tive 76; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 AGNOSIGNYRGWFNPGSVSYIY 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSEMLA----ATPKSVKAAY 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 79, Application US/11052554A; Publication No. US20050288866A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 105; Conserv
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                                                                                    GQQIQTLSSKIVARNESLKQ---QARSAQKSNAATSYINAIINSKSVSDAINRVSA--- 139
                                                                                                             122 GKRKLSLS----APQLSLKQGGLQLFSKLKPSAADQLFSAVWSDENGQDDLHWYTADADG 177
                                                                                                                                                    ---IREVVSANEKMLQQQEQD----KAAVE-QKQQENQAAINTVAAN 178
                                                                                                                                                                                      178 NTLAGYANHKGYGTYHVHTYLKQNGKMIPISAQDIDIPKPKVKIQIDKINDTSYDVVVNN 237
                                                                                                                                                                                                                          -----QETIAQNTNALNTQQAQLEAAQLNLQAE-- 206
                                                                                                                                                                                                                                                ---LTTAQDQKATL---VAQKAAAEEAARQAAAAQAAAEAKAAAEA 246
                                                                                                                                                                                                                                                                                                                           298 LSKKLDGLGETHFNVPSIINYEDPQVTIDHYNINKGTFDVTVAETDNSKAIQSISAAVWS 357
                                                                                                                                                                                                                                                                                                                                                               ----DSTEQSAAQ 295
                                                                                                                                                                                                                                                                                                                                                                                              358 DANQANLYWYEAKQLANGKAAITVDVQ-----KHGNQTGSYNVHVYVHYNDGTTSGHVL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                   296 AVNNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGVKSLAPWVGNYWGNG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQWAASAAAGYRVGSTFSAGAVAVWNDGGYGHVAYVTGVQ-GGQIQVQEANYAGNQSIG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 VAIWSEENGÖDDLKWYHASNDGSNQLTVHFNAENHGSKVGSYIAHAYITYTDGNRVGVNL 121
                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE REPERENCE: 191348018:
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATCHIN Ver. 2.1
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US-10-793-626-3244
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11.2%; Score 235; DB 6; Length 257;
Best Local Similarity 34.5%; Pred. No. 3.5e-07;
Matches 59; Conservative 29; Mismatches 75; Indels
                   ---AENQRLEAQS
                                                                                                                                                                                                                                                                                                                                                               247 KALQEQAAQAQAAANNNTQATDASDQQAAAADNTQAAQTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3244, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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|NFRGWFDPTTSYLGRLTYIYPD 544
                   GOVSALQTQQAELQ-----
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ORGANISM: Artificial Sequence
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LENGTH: 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 AAEAQKKAEAAAAALKKKAEAAEAAAAABEARKKAAAEKAAADKKA---AEKAAAEKAAADK 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GOVSALOTOQAELQAENQRLEAQSATLGQQIQTLSSKIVARNESLKQ-----QARSAQKS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SÓESS-----ÁKRSDEORKMKEÓQÁA-----EELREKQAÁEQERLKÓLEKERLAAQEÓKK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 EQSAAQAVINISDQESTTATEAQ-PSASSASTAVVTANTSSANTYPAGQCTWGVKSLAP-- 346
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                                                                                                                                                                                                                                                                                                                                                       5 ILSAVLVSGVTLSSATTLSAVKADDFDAQIASQ-----DSKINNLTAQQQAAQAQVNTIQ
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                              Query Match 10.7%; Score 226; DB 7; Length 394; Best Local Similarity 27.3%; Pred. No. 1.8e-06; Matches 108; Conservative 63; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 WVGNYWGNGGQWA-ASAAAAGYRVGSTPSAGAVAVW 381
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CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SEQ ID NO 79
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Publication No. US20050276814A1

GENERAL INPORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Microbial Technics Limited
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION WUMBER: US/10/873,528
CURRENT FILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: US/09/769,787
FRIOR FILING DATE: 1999-03-27
FRIOR FILING DATE: 1999-03-27
FRIOR FILING DATE: 1999-03-27
FRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFFWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                              US-11-052-554A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-873-528-109
                                                                                                                                                                                        LENGTH: 394
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Sequence 1682, Application US/10793626

| Publication No. US20050255478A1
| GENBEAL INFORMATION: US20050255478A1
| APPLICANT: KIMMERLY, WILLIAM JOHN
| TITLE OF INVENION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
| FILE REFERENCE: PUJ480US
| CURRENT APPLICATION NUMBER: US/10/793,626
| CURRENT PILING DATE: 1999-11-09
| PRIOR FILING DATE: 1999-11-09
| NUMBER OF SEQ ID NOS: 4472
| SEQ ID NO 1682
| LENGTH: 149
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                                                                                                                                                                                                                                                                           127 SKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQQENQAAINTVAANQETIAQNT 186
                                                                                                                                                                                                                                                                                                       286 GDSTEQSAAQAVNNSDQESTTATEAQPSASSASTAVVTANTSSANTYPAGQCTWGV-KSL 344
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                                                                                       7 SAVLVSGVTLSSATTLSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQ 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
  Length 1236;
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                                            Indels
  DB 6;
                                          90; Mismatches 190;
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39.7%; Pred. No. 2.6e-06;
tive 19; Mismatches 43
                     .2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 GNYWGNGGQWAASAAAAGYRVGSTPSAGAVA 379
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10.7%; Score 225.5; 21.5%; Pred. No. 7.2
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                                            84; Conservative
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Matches 50; Conserve
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                     Best Local Similarity
Matches 84; Conserv
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US-10-793-626-1682
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Query Match
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Sequence 211, Application US/11052554A

publication No. US20050288866A1

general information:
General information:
General information:
General information:
General information:
General information:
General information:
FILE REPERENCE:
JITLE OF INVENTION:
FILE REPERENCE:
JOES-140325A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SEQ ID NOS: 763
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                             67 FPGQVINVGGSASQNTSSNTSSSASSHTVVAGESLNIIANKYGVSVDALMQANHLNGYL 126
                                                                                                                                    127 IMPNQILTIPNGGSGSGGGTATQTSGNYTSPSFNHQNLYTEGQCTWYVFDKRSQAGKPI 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 NSKSVSDAINRVSAIREVVSANEKMLQQQEQDKAAVEQKQGENQAAINTVAANQETIAQN 185
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                                                                                        ----KSLAPWV
                                                                                                                                                                                  349 GNYWGNGGQWAASAAAAGYRVGSTPSAGAVAVWNDGGYGHVAYVTGVQG-GQIQVQEANY
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25.9%; Pred. No. 0.00014;
tive 62; Mismatches 113;
281 ---QAAQTGDSTEQSAAQAVNNSDQESTTATEAQ-
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                                                                                          -----PSASSASTAVVTANTSSA-----
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                                                                                                                                                                                                                                                                               408 AGNOSIGNYR 417
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US-11-052-554A-211
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US-10-857-780-23
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                          Sequence 2870, Application US/10793626
Sequence 2870, Application US/10793626
Publication No. US2005025478A1
GENERAL INFORMATION:
APPLICAMT: KIMMERIX, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2870
LENGTH: 157
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10.2%; Score 215; DB 6; Length 270;
1 Similarity 27.6%; Pred. No. 5.1e-06;
69; Conservative 29; Mismatches 96; Indels
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Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Pooley WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
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Matches 50; Conservative
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Best Local Similarity
Matches 69; Conservat
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US-10-485-517-413
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LENGTH: 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GVILSSATILSAVKADDFDAQIASQDSKINNLTAQQQAAQAQVNTIQGQVSALQTQQAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence US-10-793-626-3154
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APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Soster, Simon
APPLICANT: Foster, Simon
APPLICANT: Mond, James
ITILE OF INVENTION: Antigenic Polypeptides
FILE REPRENCE: P100629W0
CURRENT PILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR PILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 212
LENGTH: 1448
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR FILING DATE: 1990-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3154
LERGTH: 1095
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                  APPLICANT: KAMMEREN, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: THEREOF FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANNNTQ-----ANNNTQ-----ANDASDQQAAAADNTQAAQTGDSTEQSAA 294
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TITLE OF INVENTION: STRAHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILL REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        465 SSLITDLÓSSIŚNISQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQDQELAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REPERENCE: SEQ-4669-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SEQ ID NO 23
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Publication No. US20050255478A1
GENERAL INFORMATION:
         US20050272043A1
                                  GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-793-626-3154
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91 QTLSSKIVARNESLKQQARSAQKSNAATSYINAIINSKS-----VSDAINRVSAIRE 142
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                                                                                                                                                                                                                                                                                                                              200 QLNLQAELTTAQDQKATLVAQKAAAEEAARQAAAAQAAA---EAKAAAEAK--ALQEQAA 254
                                                                                                                                                                                                                                                                                                                                                                                          : | : | : | : | | | | : | | | | 308
253 KANAEAAINAVTPK----VVKKQAAKDEIDQLQATQINVINNDQNATTEEKEAAIQQLAT 308
                                                                                                              7 SAVLVSGVTLSSATTLSAVK----- ADDFDAQIASQDSKINNLTAQOQAAQAQV---- 55
                                                                                                                                  :| :: | :: || : || 20 NAKTINEATIAAITPDANVKPAAKQAIADKVQAQETAIDGNNGSTTEEKAAAKQQVQTEK 79
                                                                                                                                                                          56 NŢIQGQVSALQŢQQAELQAENQ----RLEA-QSAŢ-------LGQQI 90
                                              Query Match
9.1%; Score 192.5; DB 6; Length 1448;
Best Local Similarity 25.0%; Pred. No. 0.00066;
Matches 92; Conservative 60; Mismatches 147; Indels 69; Gaps
; ORGANISM: Staphylococcus aureus US-10-485-517-212
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